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Minimum
Maximum
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Maximum Match 100%
Listing first 1500
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weil, B., Amid, C., (Wiemann C.)
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Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761N011 Further information about the clone and the sequencing project : available at http://mips.gsf.de/projects/cdna/. sequenced by Medigenomix (Martinsried/Germany) within sequencing consortium of the German Genome Project. This clone (DKFZp761N011) is available at the RZPD Deu Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Neuherberg, GERMANY

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

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Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; 3381 bp mRNA DKFZp761N011 (from Ingolstaedter Landstr.1, D-85764 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Osanger, A., Deutschenbaur,S., Sc Osanger,A., Fobo,G., linear HTC 22-SEP-2004 clone DKFZp761N011). RZPD Deutsches Berlin, German Schaipp,A., 18

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/protein_id="CAD38752.1"
/db_xref="GG1:21739418"
/db_xref="GG1:21739418"
/db_xref="GA1:Q9BQIO"
/db_xref="UniProt/TrEMBL:Q9BQIO"
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89. .541
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/codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hor
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Li,W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
   Genoscope.
Direct Submission
                                     Faraday Avenue
2 (bases 1 to
                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                           GAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTG
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/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
/clone="CSODJ009YG24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced Contact; Genoscope
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2 rue Gaston Cremieux, CP 5706 -
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/organism="Homo sapiens"
/mol type="mcNA"
/mol type="mcNA"
/db xref="taxon:9606"
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/clone="CSODKO04YL21"
/cell type="HELA CELLS COT 25-NORWALIZED"
/cell line="HELA"
/cell line="HELA"
/clone lib="Homo sapiens HELA CELLS COT 25-NORWALIZED"
/clone lib="Homo sapiens HEL
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                                                                                      TGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCCAAGCCA
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n: Mismatches 2;
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93.1%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.

22 1 (bases 1 to 958)

23 Li.W.B., Gruber, C., Jessee, J. and Polayes, D.

24 Ry. B., Gruber, C., Jessee, J. and Polayes, D.

25 Full-length cDNA libraries and normalization

26 Unpublished (2001)

27 Unpublished (2001)

28 Contact: Genoscope

2 Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

28 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPRT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a material control of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence belongs to sequence cluster 5100.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODF037CH06NPl&c=5100.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL538687.3 GI:45714393
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GCCAGGGCAGGAGGCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACATTGCTAGCCTGCCCTGAGGACCCCCGCCTGGACTCCCCAGCCTTCCCACCCCATAC
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                                                                                                                                           CTCCTTCCCCGCTCCCTGTGCAGAAGGGCCTGATATCAAAACCAAAAAACTAGAGGGGGCAGG
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                                                                                                      CTCCTTCCCCGCTCCCTGTGCAGAAGGGCTGACATCAAACCAAAAACTAGAGGGGGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="FETAL BRAIN"
/dev stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primeT. Flow prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF037YP11"
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FEATURES	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 6 BX400361 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	B Q B Q	Q			
True Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5100.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ009BD12QPl&c=5100.f. Location/Qualifiers	3	BX400 BX400 BX400 BX400 BX400 BX400	1375 GAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGACTGAGAAA 1434	1256 TCCCTTACTGGGGCAGAGGGCTTCCGGAGGCAGAACTGAGGCCTGGGG-TTTCGGGGG 1314	0 0 0 0	CGGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCTCATCCTCAGTGATGTGAAG	GCCAGGGCAGGA-GCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGMACTCTCCA TCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACGACGACGACGACGACGACGACGACGACGACG
	### CITCCLISTCAMANCE CANACTACANANCE ANAMACTACANGGE CANGGE	301 Arctriccicicciriciriciaciaciaciticitica vercicicicce de la referencia	Qy 547 AGCCTGCCCTGAGGACCCCGCCTGGACTCCCCAAGCCTTCCCAACCCCATACCTCCCTC	Qy 427 TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAA 486	AGGATGATGAGAAGCTTGGTGTCCCCAAGACCCAC	ORIGIN Describes of the pCMVSPORT 6 vector. Library was normalized." ORIGIN ORIGIN Sites of the pCMVSPORT 6 vector. Library was normalized." ORIGIN 55.8%; Score 828.4; DB 5; Length 894; Best Local Similarity 96.2%; Pred. No. 1.4e-207; Matches 855; Conservative 8; Mismatches 24; Indels 2; Gaps 2;	source /organism="Homo sapiens" /do_type="mRNA" /db_xref="taxon:9606" /clone="CSDDJ009YG24" /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" /clone_lib="HOMO sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" /note="1st strand CDNA was primed with a NotI-oligo (dT)

2 4 8 4 8 4 8 4 8 4	GG 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Db Db RESULT 7 BX374861 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TIFLE JOURNAL COMMENT
20 CGGAGCCCGGACCAGGCCCTTTGCCTCCTCCTCCTCCCCGCGAGCCTCCCGAAGCCTG		8, 1, 2,
REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOUICE	Qy Qy Qy Db Qy Db RESULT 8 BM546841 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	8 8 8 8 8 8 8 8 8 8 8 8
1 (bases 1 to 1096) NIH-MGC http://mgc.nci.nih.gov National Institutes of Health, Unpublished (1999) Contact: Robert Strausberg, Pt Email: cgapbs-remail.nih.gov Tissue Procurement: Invitroger cDNA Library Arrayed by: The DNA Sequencing by: Agencourt Clone distribution: MCC clone found through the I.M.A.G.E. (http://image.llnl.gov Plate: LLAM12711 row: h colu High quality sequence stop: 66 High quality sequence stop: 66 1. 1096 //organism="Homo sapie"	680 TTTTCATC	TANAGAGGATGATGGAGAAGCTTGGTTGCCCAAGACCCACCTGGAGATGAAGAAGATGA 1

ORIGIN

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

EST 25-MAR-2004

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Query Match
Best Local Similarity
Matches 809; Conserv
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 AAGGGCTGATATCAAACCAAAAACTAGAGGGGCCAGGGCC 838
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size_2.1 kb, insert size range_1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
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/clone="IMAGE:5723574"
/lab_host="DH10B"
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98.7%;
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Pred. No. 7.9e-196;
0; Mismatches 9;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL550606
AL550606.3
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31272423.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 781)
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                                                                                         TTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCT
                                                                                                                                                                  GAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGACCTTCCAGAAAAACCTCACAGCC
                                                                                                                                                                                                                      GGGAAGGCGTTCGGCTTGAAAGCCCCGGCAGGAGGAGGCTGGCCGAGATCAACCGG
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           TTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCCACCTGGAGATGAAGAAGATG
                                                                   TTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCT
                                                                                                                                            GAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAAGCTCACAGCC
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 6.1
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Length

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Gaps

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                                                                  source
                                                                     Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Invitrogen Corp
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM583 row: j column: 10
High quality sequence start: 22
High quality sequence stop: 718.
Location/Qualifiers
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AGENCOURT 15463186 Lupski anterior horn Homo sapiens IMAGE 10516609 5', mRNA sequence.
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 832)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                 CF454825.1 GI:34454481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATCCTGAGCCTTGGGTCCCCTCCCTCTTCTTCCCCTCCTTCCCCCGCTCCCTGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:30516609"
/tissue_type="Peripheral Nervous system"
/lab_host="DH10B (T1 phage-resistant)"
                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="Lupski_anterior_horn"
/note="Vector: pCNV-SPORT6.1; Site_1: EcoRV (destroyed);
Site_2: Not1; Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 2.1 kb. Library was constructed by Invitrogen
and donated by J. Lupski, M.D./Ph.D. (Baylor College of
Medicine)."
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229 GAAGAGAACCTTCCAGAAAAAGCTCACAGCCTTCAAAGGAGAAGTACATGGAGTTTGACCTG
GGGTTTCCTTG 1019
                                              TAGA-CCCAGGCCACTCTGAGAAGACCTTGGAGTAAGGACAATGCTGCAGGGGCTCTTTC
                                                                    AGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTC
                                                                                                                                                                                          GGCAGGGCCAGGCAGGCAGGCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGCA
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                                                                                                                      CTCTCCATCCTTTCAGAAAGTCTCCAAGCCCAGTTCATGCTCACTGACCTGGCTCTGACG
                                                                                                                                           CTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACG
                                                                                                                                                                                                                                                                                                   TTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTGATATCAAACCAAAAAACTAGAGG
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842 bp

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Best Local Similarity
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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CD514425
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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High quality sequence stop: 721.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GGAGATGAAGAAGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCG
                                                                         GATTGACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCT
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/lab host="DH10B-Ton A ( T1 and T5 phage resistances)"
/lab host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone lib="NH1 MGC 181"
/clone troyed; pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:30398267"
/tissue_type="White Matter"
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|mol_type="mRNA"
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3.1e-187;
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1 (bases 1 to 755)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30659228.
                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI -oligo(dT) primer. Five prime
1st strand cDNA was diffested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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BX421987 Homo sapiens T CELLS (JURKAT CELL
clone CSODHO06YD09 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                       This sequence belongs to sequence cluster 5100.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODH006CB05QP1&c=5100.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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BX421987.2 GI:46934324
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/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned i
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                          tissue type="T CELLS (JURKAT CELL LINE"
                                                                                                                 clone="CSODH006YD09"
                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755 bp mRNA
ELLS (JURKAT CELL
                                                                                              (JURKAT CELL LINE) "
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LINE) Homo sapiens cDNA
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                                                                  781 bp
AGENCOURT 8965831 NIH_MGC_142 H
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                               Homo sapiens
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                  domo sapiens (human)
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Similarity 99.2%;
                                                                                                                                                                                                                                  AAGGGGCTCTGGGTCGGGGAATCCTGA
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Pred. No. 2.9e-182;
5; Mismatches 0;
                                                                                                                                  bp
2 Homo
                                                                                                                                                                                                                                                                  747
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                 mRNA
sapiens
                                                                                                                                  linear EST 20-SEP-2002 CDNA clone IMAGE: 6454060
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Best Local Similarity
Matches 761; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2630 row: i column: 05 High quality sequence stop: 563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                   GGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAAACCTTCCAGAAAAAGCTCACAG
                                                                                                                                                                                                                                                                     GÄGGGÄÄGGCGTTCGGCTTGCTCAAAGCCCCGGCAGGAGGAGGAGGCTGGCCGAGATCAACC
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                                                                                                                                                                                                   GGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAAGCTCACAG
                      TGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAACA
                                                                                                 CTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCCACCTGGAGATGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="mixed (pool of 40 RNAs)"
/lab_host="DH108 (T1-phage-resistant)"
/clone lib="NIH MGC 142"
/note="Wector: pDNR-LIB; Site 1: SfiI (ggcgattatggcc);
/note="Wector: pDNR-LIB; Site 1: SfiI (ggcgattatggcc);
/site 2: SfiI (ggcggcttgggc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2*, blood - 33.4*, brain - 5.6*, breast - 12.5*, colon - 4*, connective tissue - 1.4*, eye - 1*, intestine - 2.6*, kidney - 2.2*, liver - 5.7*, lung - 10.8*, NK-cell - 5.2*, ovary - 4*, pharynx - 2.5*, prostate - 4.3*, salivary gland - 1.3*, and skin - 2.3*). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGGCCATTACGGCCGGG-3' and 5'-ATTCTAGAGGCCGAGAGTGGCCATTCGGCCGGG-3' and 5'-ATTCTAGAGGCCGAGAGTGGCCATTCGGCCGGG-3' and 5'-ATTCTAGAGGCCGAGAGTGGCCACATC-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech creation (other fractions present in NIH MGC 141).
Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE: 6454060"
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Pred. No. 1.3e-178;
0; Mismatches 12;
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Gaps

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RESULT 14
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                                                                                                                                                                                                                                                                        Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa M
Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  724
                                                                                                                                                                       Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.ppenbiosystems.com).
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 701)
Bonaldo,M.F., Lenmon,G. and Soares,M.B.
Normalization and subtraction: two approaches to faci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA312962
CA312962.1 GI:24531060
EST.
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                                                                                                                                                                                                                                                                                                                                                                                         discovery
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                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: M13 FORWARD
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="UI-CF-FN0-aex-g-19-0-UI"
/clone="UI-CF-FN0"
/lab host="DH10B (Life Technologies) (T1 phage resistant)
/lab host="DH10B (Life Technologies) (T1 phage resistant)
/clone lib="UI-CF-FN0"
/clone lib="UI-CF-FN0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
                                                                                                                                      ocation/Qualifiers
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TRG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
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	y Match Local Similarity 98.9%; Pred. No. 5.2e hes 693; Conservative 0; Mismatches	y Match Local Similari hes 693; Cons	Pax: 81-438-52-3986 Email: genomics@hri HRI human cDNA projon Research Institute; Virology, Institute Helix Research Institute Coation/Qy Ource // 1701 Ource // 1701 Ource // 1701 Coll type= // 2. // 2	Genomics Laboratory Helix Research Inst. 1532-3 Yana, Kisara: Tel: 81-438-52-3976 Email: genomics@hri HRI human cDNA proj. Research Institute; Virology, Institute; Virology, Institute; Virology, Institute Helix Research Inst. ES (1701 Ource (700) Ource (7
HRI human cDNA projections of the control of the co	HRI human cDNA projection, K., Yamamoto, Saito, K., Yamamoto, Sugano, S., Masuho, Y. Sugano, S., Masuho, Y. Al. Unpublished (2000) Conteact: Takao Isogg Genomics Laboratory Helix Research Inst. 1532-3 Yana, Kisara: Tel: 81-438-52-3975 Fax: 81-438-52-3975 Fax: 81-438-52-3976 Fax: B1-438-52-1086 Fax: B1-438	HRI human cDNA project (Ota,T., Sugiy Saito,K., Yamamoto,J., Nishikawa,T., Sugino,S., Masuho,Y., Isogai,T.) AL Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812 Tel: 81438-52-3975	HRI human cDNA project (Ota,T., Sugiy Saito,K., Yamamoto,J., Nishikawa,T., Sugano,S., Masuho,Y., Isogai,T.) AL Unpublished (2000)	

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3: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*

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Patent No. 6135941

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Nu-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-09-049-672A-16
                                                             US-09-049-672A-16
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C1498
C1499
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE: HEREWITH
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, I.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                              STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOTO4
CLONE: 1320068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-855-0555
                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                         TELEFAX: 650-845-4166
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US-09-252-991A-7471
US-09-902-540-6405
US-09-902-540-6405
US-08-118-200-1
US-08-48-745-1
US-08-48-745-1
US-08-819-254-8
US-09-030-270A-8
US-09-030-270A-8
US-09-031-587-8
US-09-031-587-8
US-09-031-587-8
US-09-431-614-16
      Score 1445.6;
Pred. No. 0;
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                       DB
                     Length 3449;
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INAME! AND INFORMALIAN: NAME: JORATHAN L. Klein REGISTRATION NUMBER: 41,119 REFERENCE/DOCKET NUMBER: PF353 TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504 INFORMATION FOR SEO ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 632 base pairs TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: linear	COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: COMPARIBLE PC-DOS/MS-DOS SOFTWARE: PATENTIN PC-DOS/MS-DOS SOFTWARE: PATENTIN PC-DOS/MS-DOS CURRENT APPLICATION NUMBER: US/09/010,147B FILING DATE: 12-No. 6653445-2002 CLASSIFICATION: <unknown> PRIOR APPLICATION NUMBER: US 60/034,205 FILING DATE: 21-UN-1997 APPLICATION NUMBER: US 60/034,204 FILING DATE: 21-UN-1997 APPLICATION NUMBER: US 60/034,204 FILING DATE: 1-UN-1997 APPLICATION NUMBER: US 60/034,204</unknown>	RESULT 2 US-09-010-147) Sequence 11 Fatent NO. GENERAL II GENERAL II INUMB! CORRI	1; Qy 1087 GCTGATCCCCACTCATTCCACACCTCTTCTCATGCTAAAGGTGGAAGGAA

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RESULT 3
US-08-361-441B-43
US-08-361-441B-43
; Sequence 43, Application US/08361441B
; Patent No. 6077948
; GENERAL INCORMATION:
APPLICANT: RUBBELL, MARY E.
APPLICANT: Utens, Ulrike
TITLE OF INVENTION: MEDIATORS OF C!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 88.537
; SEQUENCE DESCRIPTION: SE US-09-010-147B-11
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STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                     NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                           STREET: 225 F
CITY: Boston
STATE: MA
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                                                                          225 Franklin
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Pred. No. 5.4e-159;
0; Mismatches 2;
                                                                                                                                   OF CHRONIC ALLOGRAFT REJECTION
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                                                                                      RESULT 4
US-08-792-013-5
; Sequence 5, Application US/08792013
; Patent No. 6204021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 491 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.9%;
Best Local Similarity 67.1%;
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Murry, Lynn E.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/361,44
PRIOR DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
PILLING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/0
TELECOMMUNICATION INFORMATION:
TELECHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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'STRANDEDNESS: dou
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 TTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGAGGCTGGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATGTCCCTGAAACGAATGCTGGAGAAACTTGGAGTCCCCAAGACTCACCTAGAGCTA
                                                                                                                                                                                              CIGCCCIGA
                                                                                                                                                                                                                                                                                                   CTCAGGATGATGCTGGGCAAGAGATCTGCCATCCTAAAAATGATCCTGATGTATGAGGAA
                                                                                                                                                                                                                                                                                                                    GTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGA
                                                                                                                                                                                                                                                                                                                                                              AAGAAATTAATTGGAGAGGTGTCCAGTGGCTCCGGGGAGACGTTCAGCTACCCTGACTTT
                                                                                                                                                                                                                                                                                                                                                                               AAGAAGATGATCTCAGAGGTGACAGGAGGGGGTCAGTGACACTATATCCTACCGAGACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGAAGGCTTCAAAGAGAAATACATGGAGTTTGACCTTAATGGAAATGGCGATATTGAT
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                                                                                                                                                                               TIGCCCIGA
                                                                                                                                                                                                                                        AAAGCGAGAGA---AAAGGAAAAGCCAACAGGCCCCCCCAGCCAAGAAAGCTATCTCTGAG
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
                                                                                                                                                                                                          558
                                                                                                                                                                               468
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   HUMAN CYTOKINES
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Pred. No. 9.6e-44;
0; Mismatches 138;
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ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 base pairs
TYDE: nucleic acid
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Best Local Similarity
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APPLICATION NUMBER: US/08/792
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PAI
STREET: 3174 Porter DI
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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SOFTWARE: FastSEQ for Windows Version
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CLONE: 815614
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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3174 Porter Drive
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Pred. No. 1.1e-43;
0; Mismatches 138;
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3906
LENGTH: 658
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NAME/KEY: misc feature
LOCATION: 525
OTHER INFORMATION: n=a,
US-09-513-999C-3906
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59. US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3906, Application US/09513999C Patent No. 6783961 GENERAL INFORMATION:
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Best Local
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NAME/KEY: CDS
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ORGANISM: Homo sapiens
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284; Conserv
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Pred. No. 6.1e-42;
0; Mismatches 141;
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RESULT 6 US-09-513-999C-14979 ; Sequence 14979, Application US/09513999C ; Patent No. 6783961

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FILE OF INVENTION: Expressed Sequence Tags and Enc. Patcent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patcent.pm
SEQ ID NO 14979
                                                                                                                     RESULT 7
US-08-361-441B-4
Sequence 4, Application US/08361441B
Patent No. 6077948
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                       GENERAL INFORMATION:
APPLICANT: RUSSEll, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 464
OTHER INFORMATION: n=a, g
IS-09-513-999C-14979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards,
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
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TYPE: DNA
  ADDRESSEE: Flo...
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Pred. No. 3.6e-41;
0; Mismatches 139;
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                                                                   CHRONIC ALLOGRAFT REJECTION
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                                                      RESULT 8
US-08-171-385-4
Sequence 4, Application Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. R
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US-08-361-441B-4
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TELERAX: 61//--
TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ RNGTH: 627 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/08/361,441B
FILLING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILLING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                        ATTGCTAGCCTGCCCTGA 558
                                                                                                               TCTGACTTTCTCAGAATGATGCTGGGCAAGAGATCTGCCATCTTGAGAATGATTCTGATG
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                                                                                    TATGAGGAGAAAAACAAAGA---ACACCAGAAGCCAACTGGTCCCCCAGCCAAGAAAGCT
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Pred. No. 2.2e-40;
0; Mismatches 151;
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US/08171385

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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS. Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ulrike Ut TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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ATTGCTAGCCTGCCCTGA 558
                                                                                                             CGAGACTTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATG 480
                                                                                                                                                                  CTGGAGATGAAGAAGATGATCTCAGAGGTTGACAGTGAGGGGGTCAGTGACACTATATCCTAC
                                                                                                                                                                                                    GATATCGATATTATGTCCTTGAAGCGAATGCTGGAGAAACTTGGGGTTCCCAAGACCCCAT 319
                                                                                                                                                                                                                            GAGATTGACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCAC
                                                                                                                                                                                                                                                                                TTGGATGGGATCAACAAGCACTTCCTCGATGATCCCAAGTACAGCAGTGATGAGGATCTG
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                                                                TCTGACTTTCTCAGAATGATGCTGGGCAAGAGATCTGCCATCTTGAGAATGATTCTGATG
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                                       TATGAGGAGAAAAACAAAGA ---ACACCAGAAGCCAACTGGTCCCCCAGCCAAGAAAGCT
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VENTION: Mediators of Chronic Allograft
VENTION: Rejection
SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Pred. No. 2.3e-40;
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FILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOCTWARE: Patent.pm
SEQ ID NO 10617
LENGTH. 50.00
                                                 Sequence 1, Application US/08171385
Patent No. 5527884
PATENTAL INFORMATION:
APPLICANT: Wary E. Russell
APPLICANT: Ulrike Utans
ITILE OF INVENTION: Mediators of C
ITILE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards,
APPLICANT: Duclert, A.
APPLICANT: Diclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed So
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
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US-09-513-999C-10617
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US-09-513-999C-10617
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US-08-171-385-1/c
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Best Local Similarity
Matches 205; Conserv
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NAME/KEY: misc_feature
LOCATION: 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 507
STREET:
                   ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 ATCATGTCCCTGAAACGAATGCTGGAGAAACTTGGAGTCCCCAAGACTCACCTAGAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCGAGAGA---AAAGGAAAAGCCAACAGGCCCCCCCAGCCAAGAAAGCTATCTCTGAG 391
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                                                                                                                        Mediators of Chronic Allograft
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Pred. No. 1.2e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COUNTRY:

02110-2804

STATE: Massachusetts

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RESULT 11
US-08-361-441B-1/c
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                                                                                                                                                                                                                                                      Sequence 1, Application US/08361441B Patent No. 6077948
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Best Local Similarity
                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
                                                                                                                                                                  APPLICANT: RUSSell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                              NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                       STREET: 225 F:
CITY: Boston
STATE: MA
                  COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 331
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 TCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCAACGAGAGCAGCCAAGCCAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 TTGGTGTCCCCAAGACCCCACCTGGAGATGAAGAAGATGATCTCAGAGGTGACAGGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                              521 GCCCCCCCCAGAGAGAGACATTGCTAGCCTGCCCTGA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 CCGAGGAGACGTTCAGTTACTCTGACTTTCTCAGAATGATGCTGGGCAAGAGATCTGCCA 147
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                                                                                              225 Franklin Street
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Pred. No. 1.7e-16;
0; Mismatches 97;
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-337,768
PRIOR FILING DATE: 2000-10-39
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US-09-949-016-5139
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5139, Ap
Patent No. 681233
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Best Local Similarity 63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fraeer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1'
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Pred. No. 1.7e-16;
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OF DETECTION AND USES THEREOF
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RESULT 14
US-09-949-016-16881
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US-09-949-016-5140
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US-09-949-016-5139
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
                                                                                                                                             Sequence 16881, Application US/09949016 Patent No. 6812339
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
TILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5140
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Best Local Similarity
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TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                  TTTGTGAACATGATGCTGGGGGAAACGGTCGGCTGTCCTCAA 467
                                                                                                                                                                                                                                                                                                                                                           CTAAAGAAATTAATTGGAGAGGTGTCCAGTGGCTCCGGGGAGACGTTCAGCTACCCTGAC
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Pred. No. 7.7e-12;
0; Mismatches 51;
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                                                                AND USES
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-16882
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US-09-949-016-16882
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; ORGANISM: Human
US-09-949-016-16881
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SOFTWARE: FastSEQ for
SEQ ID NO 16882
LENGTH: 5502
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GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
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TTTCTCAGGATGATGCTGGGCAAGAGATCTGCCATCCTAAA 2983
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                                                             TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAA 467
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                                                                                                                ABL88176 standard; cDNA; 149
Human PRO1306 cDNA sequence
WC200200690-A2.
                                                                                                                                                                                                          ABK33590 standard; cDNA; 1485 BP. cDNA encoding human PRO protein, WO200208288-A2.
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DNA encoding protein of the invention
WO200078961-A1.
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Human PRO1306 (UNQ672) cDNA sequence
                       WO200208284-A2.
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Human angiogenesis related cDN
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         Novel human secreted and US2003073129-A1.
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06-MAR-2003.
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Human secreted/transmembrane polypeptide PRO 1306
US2003044934-A1.
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Human PRO1306 cDNA.
US2003027988-A1.
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Novel human secreted and transmembrane
US2003073130-A1.
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13-MAR-2003.
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                                                                                                   Human cDNA encoding
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Human cDNA encoding secreted/transmembrane
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Human PRO1306 cDNA
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HILLAN K J.
MARSTERS S A.
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Novel human secreted and
US2003096968-A1.
22-MAY-2003.
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Human PRO polynucleotide #55.
US2003073817-A1.
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Novel human secreted and transmembrane
US2003092886-A1.
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US2003092890-A1.
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Novel human secreted and transmembrane
US2003069397-A1.
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Novel human secreted and
US2003092887-A1.
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22-MAY-2003.
(GETH ) GENENTECH INC.
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Human PRO polynucleotide #55.
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                                                               ADD70710 standard; cDNA; 1485
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US2003099625-A1.
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Novel human secreted and
US2003073816-A1.
17-APR-2003.
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ADD51265 standard; cDNA; Novel human secreted and US2003105289-A1.
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        Novel human secreted US2003045687-A1.
                           ACD68647 standard; cDNA; 1485
                                                                                      US2003036635-A1.
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Human cDNA encoding secreted/transmembrane
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Human PRO polynucleotide
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Novel human secreted and transmembrane protein US2003092888-A1.
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                 ADE39034 standard; cDNA; 1485
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Novel human secreted and transmembrane
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US2003100064-A1.
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Novel human secreted and
US2003100733-A1.
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Novel human secreted and transmembrane
US2003100732-A1.
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Human PRO polynucleotide #55.
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Novel human secreted and
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Human PRO polynucleotide #55.
US2003100726-A1.
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                                     ADD77590 standard; cDNA;
Novel human secreted and
US2003100729-A1.
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Novel human secreted and trans
US2003100719-A1.
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Novel human secreted and trans
US2003100731-A1.
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Human PRO polynucleotide #55.
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Novel human secreted and transmembrane
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                                         Human cDNA encoding US2003195347-A1.
                                                 ADE96568 standard; cDNA; 1485 BP.
Human cDNA encoding secreted/transmembrane
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                                          Novel human secreted and 252-MAY-2003
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ABA93720 standard; cDNA; 3381 BP. Human differentiation/development WO200198454-A2.
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Human cDNA encoding secreted/
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No. 0;
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No. 0;
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No. 0;
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CDNA

clone amy2_1j19

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Lery Match
Best Local Similarity
RESULT 123
ID ACM38972 star*
DE Tumour-*
PD W02^^
Query Match
Best Local '
RESULT 13'
ID
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DE
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Best Local Similarity
RESULT 124
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RESULT 1
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RESULT
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Best Local Similarity
RESULT 130
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Tumour-associated antigenic target
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(GEHU-) GERMAN HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated protein US6135941-A.
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5-APR-2004.

(GETH ) GENENTECH INC.

97.4%;

99.7%;
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WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC66521 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide WO200153312-A1.
                                                                                                                                                        Breast cancer prognosis marker #2540.
W02004065545-A2.
                                                                                                                                                                                                                                Full length human cDNA useful EP1447413-A2.
                                                                                                                                                                                                                                                                                                          WO200240672-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI58050 standard;
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(INCY-) 97.3%;
ry Match 97.7%;
r Local Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                   ABT03024 standard;
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                 .8-AUG-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
ry Match 92.6%; Score
ry Match 94.9%; Pred.
                                                                                                                                                                                                                                                                                                (DIAD-) DIADEXUS INC.
     ANI96213 standard; cDNA; 768 BP. Human neuroblastoma expressed polynucleotide
                                                                                WO200166719-A1.
                                                                                        Human neuroblastoma
                                                                                                 AAI96212 standard;
                                                                                                                                    (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
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                                 Local Similarity
                                                                                                                                                                                                                                                                            ocal Similarity
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                                 PHARM CO LTD.
43.4%; Sc
y 97.0%; Pr
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de SEQ
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97.8%;
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99.1%;
                                                                                        expressed
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99.1%;
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99.7%;
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for treating
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No. 0;
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No. 0;
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No. 0;
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No. 0;
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. No. (
                                   644.4; DB 4;
No. 5.3e-169;
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Best Loc
RESULT 138
ID ABTO?
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PN W'
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Best Local Similarity
RESULT 132
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RESULT 1
RESULT 139
ID ABL499
DE Intrac
PN WO2002
PD 07-FEB
PA (KYOW
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RESULT 137
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Best Local S
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21Y Match 41.5%;
3t Local Similarity 92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA clone
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(HISM ) HISAMITSU PHAM CO LTD.

43.0%; So
ry Match 43.0%; So
t Local Similarity 93.5%; Pi
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                                                                                                                                                                                                                                                                                                                                      ABL49913 standard; DNA Intracellular calcium WO200210371-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV41919 standard; cDNA;
                                                                                                                                                                     Human cDNA sequence #121 w0200279411-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GEN
(AUCK-) AUCKLAND
                                                                                                                                                                                                                                                                   AAV82798 standard; cDNA; 453 BP.
cDNA encoding a ATG-1117 (allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal brain
                                                                                                Human breast specific WO200240672-A2.
                                                                                                                                                                                                                                                             EP879880-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      (STAC/) STACHE-CRAIN
                             ABL49912 standard; DNA; 444 BP.
Intracellular calcium ion transport
                                                                                                                     ABT03023 standard;
                                                                                                                                                                                                                                        (SMIK) SMITHKLINE
                                                                              23-MAY-2002.
(DIAD-) DIADEXUS INC.
                                                                                                                                                         LO-OCT-2002.
(VAND-) VAN ANDEL INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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ch 30.4%;
l Similarity 99.8%;
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JONES L W.
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AUCKLAND UNISERVICES
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LABAT I.
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(5'-primer)
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CDNA #1180.
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30.2%; Score
99.3%; Pred.
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96.4%;
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down-regulated
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ng sequence
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Score
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Pred.
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Pred. No. 4.1e-122;
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Pred.
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Pred.
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No. 4.
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No. 2.8e-167;
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No. 3e-
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No. 2.1e-
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No.
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No.
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..7e-161;
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.3e-114;
                                                               ; DB 6;
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BB
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                                 DNA sequence SEQ
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WO200210371-A1.

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RESULT 141
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Best Local Similarity
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                                                                                                                ABK15589 standard; cDNA;
DNA encoding novel human
US2002001827-A1.
                                                                                                                                                                                                   AAD05035 standard; cDNA; 659 BP.
Novel human cytokine-2 (NHC-2) cDNA.
US6204021-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human allograft inflammatory WO9517506-Al.
                                       ADA67731 standard; DNA; 659 BP. Novel human cytokine 2, NHC-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT64809 standard; cDNA; 635 BP.
Human RC-9 cDNA useful in proliferative
WO9722880-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA65628 standard; cDNA; 491 Human allograft inflammatory US6077948-A.
                                                                                                                                                                                          20-MAR-2001.
                                                                                                                                                                                                                                           (CLIN-) CLINGENIX INC.
12.9%;
ry Match 12.9%;
t Local Similarity 67.1%;
                                                                                                                                                                                                                                                                                         WO200298355-A2.
                                                                                                                                                                                                                                                                                                  ADA19323 standard; cDNA; 639 BP.
Human insulin resistance marker IRM228
                                                                                                                                                                                                                                                                                                                                                                                    AAV82802 standard; cDNA; 635 BP.
ATG-750/RC-9 (allograft inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV82800 standard; cDNA; 635 BP.
ATG-750/RC-9 (allograft inflammatory
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- rocal Similarity 67.1%;
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ry Match 12.9%;
r Local Similarity 67.1%;
                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
ry Match 12.9%;
Local Similarity 67.1%;
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                                                                                             INCY-) INCYTE PHARM
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 GENOMICS INC.
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12.9%;
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cytokine-2
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c) Score
c) Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                Score 192.2; DB 2; Pred. No. 7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP. factor 1 (AIF-1) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                          Score 192.2; DB 4;
Pred. No. 7.9e-43;
                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192.
                                                                                                                                                                                                                                            192.2; DB 1
No. 7.7e-43;
 192.2;
                                         #2
                                                                        192.2; DB 6;
No. 7.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                    192.2; DB 2;
No. 7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192.2; DB 6;
No. 6.4e-43;
                                                                                                                            (NHC-2),
                                                                                                                                                                                                                                                                                                                                                                                     factor-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AIF-1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oΝ
                                                                                                                                                                                                                                                                                                  (AIF1) CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 2;
.8e-43;
                                                                                                                                                                                                                                                       DB 10;
 멂
                                                                                                                            version
 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease
Length
                                                                                Length
                                                                                                                                                                     Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 444;
                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 491;
                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA SEQ ID NO:43.
 659;
                                                                                                                                                                                                                                                                                                                                           635;
                                                                                                                                                                                                                                                                                                                                                                                                                              635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491;
                                                                                                                                                                                                                                                      639;
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Best Local Similarity
RESULT 155
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 154
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
RESULT:153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
RESULT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 149
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                       ABK15587 standard; of DNA encoding novel lus2002001827-A1.
                                           Human secreted EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                   ADR52830 standard; DNA; 639 Drug therapy altered express WO2004072265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR24778 standard; DNA; 639 BP. Breast canner prognosis marker WO200406545-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA differentially WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human soft tissue WO2004048938-A2.
                                                                  AAC03908 standard;
                                                                                                            (INCY-) INCYTE PHARM
                                                                                                                                                                                                  (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH ) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                                Human Mphi type
JP2001078775-A.
                                                                                                                                                                                                                                                         AAH25798 standard; DNA; 441
Human Mphi type ibaI DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE-) ROSETTA INPHARMATICS (NECA-) NETHERLANDS CANCER IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003031650-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA89946 standard; cDNA; 639 BP. Gene differentially regulated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK84357 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEIN DESIGN LABS
xy Match 12.9%;
t Local Similarity 67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ22610 standard;
                                                                                                                                                                                                                                                                                                                                                   (AMHP ) WYETH.
(BURC/) BURCZYNSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC
                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 local Similarity
                                                                                                                                                                                                                                                                                                                 DORNER A J.
                      GENSET.
                                                                                                                                                                                                                                                                                                                                         TWINE N.
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAYER AG.
                                                     ard; cDNA;
protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sarcoma-upregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%;
68.7%;
                                                                                                                                            cDNA; 658 BP.
human cytokine-2
                                                                                                                                                                                                                                                                                                                   Σ
                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%; Sco. 68.7%; Pre
                                                                                      12.6%;
65.2%;
                                                                                                                                                                            12.7%;
66.9%;
                                                                                                                                                                                                                                                                                           12.9%;
68.7%;
                                                                                                                                                                                                                                                                                                                                                                                              NA; 639 BP. expressed
12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.9%;
68.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760
                                                     658 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 192.
Pred. No.
                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B₽.
                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLC.
                                                                                       Score
Pred.
Score
Pred.
                                                                                                                                                                             Score 189.2; DB 4;
Pred. No. 4.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                            Score 191; DB 13; Pred. No. 1.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 191; DB 8; Pred. No. 1.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #639.
                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular
186;
No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                               191;
No. 1.
                                                                                       186.8; DB 6
No. 2.5e-41;
                                                     Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191; DB 6;
No. 1.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                #181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in
                                                                                                                                              (NHC-2)
                                                      ő
                                                                                                                                                                                                              SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2; DB 12;
8.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9e-43;
DB 3;
.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
.7e-42;
                                                                                                                                              version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                               HS
                                                                                                6,
         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ü
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ВP

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Best Local Similarity
RESULT 165
ID AAH25805 standard; D)
DE Murine ibaI(1-120) D)
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BBBB
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
RESULT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 159
                                                                                                                                                              RESUL
                                                                                                                                                                                                                                               RESULT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 158
                                                                                                                                                                                                                                                                                           Human insulin resistance marker W0200298355-A2.
                                                                                                                                                                                                                                                                                                                                                                                      AAA65591 standard; cDNA; 627 BP.
Rat allograft inflammatory factor 1
US6077948-A.
                                                                                                                             Murine ibaI(EF1-EF1) DNA. JP2001078775-A.
                                                                                                                                                                                                                          Rat RC-9 cDNA useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003064624-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB58279 standard; DNA; 653 Toxicity-related gene, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ99370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH25799 standard; DNA; 44 Murine Mphi type ibaI DNA. JP2001078775-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC10904 standard; cDNA;
                                                                                   (KOKU-) KOKURITSU SEISHIN SHINKEI
(IYAK-) IYAKUHIN FUKUSAYO HIGAI K)
(MOCH ) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                      AAT64808 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD) HARVARD COLLEGE.

(YARD) 12.3%;

TY Match 12.3%;

Tonal Similarity 65.1%;
                                                                                                                                                                                                                  WO9722880-A1.
                                                                                                                                                                                                                                                                                                                                             (HARD ) HARVARD COLLEGE.
ry Match 12.1%;
t Local Similarity 64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH ) MOCHIDA PHARM CO LTD.
                                                                                                                                                   AAH25804 standard; DNA; 441
                                                                                                                                                                                            SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                              (CLIN-) CLINGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
  KOKURITSU SEISHIN SHINKEI CENT SOCHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lard; cDNA; 627 BP.
inflammatory factor 1 (AIF-1) cDNA
                                                                                                                                                                                                                          cDNA; 696
ul in proli
                                 DNA;
                                                                                                                                                                                            BEECHAM
                                                                                                                                                                        11.9%;
65.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
                                                               11.3%;
                                                                                                                                                                                                                                                          12.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 653 BP.
SEQ ID 3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
                                            360
                                                                                                                                                                                                                           ; 696 BP.
proliferative
                                                                                                                                                                       ( CORP.
b; Score
b; Pred. 1
                                                                                                                                                     BP.
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                                            ΒP
                                                                                                                                                                                                                                                           Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                IRM228
                                                                                                 KYUSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  182;
No. 5.
                                                                167.8;
No. 4.2
                                                                                                                                                                        176;
No. ;
                                                                                                                                                                                                                                                           177.
                                                                                                                                                                                                                                                                                                                                              180.4;
No. 1.5
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                     (AIF-1)
                                                                                                                                                                                                                             arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:
                                                                                                                                                                                                                                                          7.8; DB 10;
7.4e-39;
                                                               7.8; DB 4;
4.2e-36;
                                                                                                                                                                                                                                                                                                                                              1.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2; DB
4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2; DB 3;
2.4e-40;
                                                                                                 SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KENKYU
                                                                                                                                                                                                                                                                                                               (AIF1)
                                                                                                                                                                         DB 2;
.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                  . 5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14979
                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
-40;
                                                                                                                                                                                                                                                                                                                                                                                                  encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS
                                                                                                 HS
                                                                                                                                                                                                                             disease
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                                                                                                                                                                                                                           diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                     NO:4.
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Best Loc
RESULT 172
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH25800 standard;
Murine ibaI(1-115)
                                                                                                                                                                                                                                                                                                                                      AAV82799 standard; c
ATG-1100 (allograft
EP879882-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein 5' EP1033401-A2. 06-SEP-2000. (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH25803 standard; DNA; 441 BP.
Murine ibaI(EF2-EF2) DNA.
JP2001078775-A.
AAT64807 standard; DNA; Rat RC-9 gene useful in WO9722880-A1.
                                                                                                     ADA67729 standard; DNA;
Novel human cytokine 2,
US2003096371-A1.
                                                                                                                                                                                                                                  AAH25802 standard; DNA; 273
Murine ibaI(30-120) DNA.
JP2001078775-A.
                                                                                                                                                                               (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH) MOCHIDA PHARM CO LTD
                                                                                                                                                                                                                                                                                    (SMIK) SMITHKLINE BEECHAM (
ry Match 8.8%;
t Local Similarity 66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOCH ) MOCHIDA PHARM CO LTI
ry Match 11.0%;
t Local Similarity 68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOCH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU
                                                (INCY-) INCYTE GENOMICS INC.
ry Match 8.5%;
t Local Similarity 65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC06542 standard; cDNA; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2001078775-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH25801 standard; DNA; 354
Murine ibaI(30-147) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOKURITSU SEISHIN SHINKEI CENT
IYAKUHIN FUKUSAYO HIGAI KYUSAI
MOCHIDA PHARM CO LTD,
MOCHIDA PHARM CO LTD,
16 9.6%; Score 143.
Similarity 64.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOCHIDA PHARM CO LTC
h 11.2%;
Similarity 67.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 345
                                                                                                                                                                                                                                                                                                                                                     cDNA; 579 BP. inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%;
                                                                                                                                                          8.6%;
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                                                                                                                  639 BP.
NHC-2, I
             1678 BP. proliferative arterial
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                                                                                                                                                                                                                                                                                      CORP.
; Score
; Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166.8; DB 4; Pred. No. 7.1e-36;
                                                    Score
Pred.
                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 143.2; DB 4
Pred. No. 2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                       factor-1gamma)
                                                                                                                                                          127.8;
No. 4.8
                                                                                                                                                                                                                                                                                         131
No.
                                                                                                                                                                                                                                                                                                                                                                                            131.4; DB 3;
No. 6.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159.8; DB 4;
No. 7.1e-34;
                                                    126.4; DB 9;
No. 1.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ħ
                                                                                                                                                                                               C SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOCHO.
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                                                                                                                                                                                                                                                                                         .4; DB 2;
6.9e-26;
                                                                                                                                                                                                                                                                                                     .4;
                                                                                                                                                           4.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10617.
                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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                 diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441;
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Best Local Similarity
RESULT 179
ID AAV82801 standard; c
DE ATG-1120 (allograft
PN EP879883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
ID AC
DE HU
PN US
PD 17
PA (I
                                                                                              BESULT 181
                                                                                                                                                                                     RESULT 180
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                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                  AAQ99371 standard; cDNA; 331 BP. Rat allograft inflammatory factor 1 W09517506-A1.
                                                                                                                                                                                                                                        AAV82801 standard; cDNA; 631 BP.
ATG-1120 (allograft inflammatory factor-1-delta)
EP879883-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 10806. W0200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT64806 standard; DNA; 424
Rat RC-9 DNA useful in prol:
WO9722880-Al.
                                                                                                                                                              ABL49900 standard; DNA; 117 BP. Intracellular calcium ion transport
                                                                                                                                                                                                                                                                                                                                         ABL49899 standard; DNA; 117 BP.
Intracellular calcium ion transport related
AAA65588 standard; cDNA; 331
                                                                                                                                                     WO200210371-A1.
                                                                                                                                                                                                                                                                                                                                WO200210371-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Renal toxin progression gene marker #1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP72830 standard; DNA; 424 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human foetal kidney 
US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACH42742 standard, cDNA;
                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
ry Match 7.7%; Sco
Local Similarity 59.7%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK) SMITHKLINE BEECHAM CORP.
ry Match 7.9%; Score
Local Similarity 64.6%; Pred.
                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KI
7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                               KYOW ) KYOWA HAKKO
                                                                                                         ocal Similarity
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                    ocal Similarity
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A/) LABAT I.
C/) STACHE-CRAIN I
                  HARVARD COLLEGE.

h 6.4%;
Similarity 63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMITHKLINE
                                                                                                       7.0%;
93.2%;
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66.2%;
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                                                                                                                                                                                                                                                                                    100.0%;
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proliferative
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1 #276.
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Pred.
 BP.
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Pred.
                    Score
Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                    117;
. No.
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No.
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No.
                    94.8;
No. 8
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No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                117.8; DB 2;
No. 3.7e-22;
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No.
                                                                          (AIF-1)
                                                                                                                                                              related
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                                                                                                                                                                                               .2; DB 2;
4.5e-21;
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3.5e-22;
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                     8
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                                                                                                          ; DB 6;
.2e-18;
                                                                                                                                                                                                                                                                                    DB 6; I
3.2e-22;
                    DB 2;
.5e-16;
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                                                                          partial
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Best I
                                Best Local Similarity RESULT 190
                                                                                                                     Query Match
Best Local Similarity
RESULT 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                       Breast cancer prognosis marker #1093. W02004065545-A2. 05-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour-associated a WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL49901 standard; DNA; 117 BP. Intracellular calcium ion transport W0200210371-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE.
PYY Match 6.4%;
It Local Similarity 63.7%;
                                                                          ABK84756 standard; cDNA; 81800 BP. Human cDNA differentially expressed WOZ00228999-A2.
      AAX89526 standard; on Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference mRNA sequences for WO2004042346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat allograft inflammatory
WO9934814-A1.
                                                                                                                                (ROSE-) ROSETTA IMPHARMATICS LLC.
(NECA-) NETHERLANDS CANCER INST.

TY MATCH

Local Similarity 68.3%; Score

Local Similarity 68.3%; Pred.
                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                ADQ83815 standard; cDNA; 1363 BP.
Human tumour-associated antigenic target
                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP10462 standard; DNA; 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP10331 standard; DNA; 1363 BP.
Reference mRNA sequences for marker
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                                                                                                                                                                                                                                                                                                     √02004060270-A2.
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ry Match 5.3%; Score
t Local Similarity 68.3%; Pred.
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h 5.3%; Score
Similarity 68.3%; Pred.
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                                                                GENE LOGIC
         cDNA; 1235
e of Interfe
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85.3%;
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                                         5.3%;
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           Interferon
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l antigenic
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marker
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Pred.
          Responsive Transcript-1
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No. 3
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No. 3.
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No. 3.
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No. 2.
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8;
                                                                                               granulocytic
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                                                                                                                                DB 13;
.4e-11;
                                            DB 6;
.6e-10;
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.4e-11;
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.4e-11;
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.4e-11;
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.4e-14;
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.5e-16;
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Best Local Similarity RESULT 198
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Best Local Similarity
RESULT 191
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RESULT 194
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                                                                                                                                  19-SEP-2001.
19-SEP-2001.
(SHAN-) SHANGHAI INST ONCOLOGY.
(SHAN-) SHANGHAI INST ONCOLOGY.
4.6%; Score
59.9%; Pred.
                                                                                          ADB47517 standard; cDNA; 1924 BP.
Human cDNA upregulated in dendrit
US2003134283-A1.
                                                                                                                                                                             CN1313316-A.
                                                                                                                                                                                       ABA04457 standard; cDNA; 1923
Human PP3051 protein encoding
                                                                                                                                                                                                                                                                ACN37848 standard; cDNA; 18:
Tumour-associated antigenic
WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                      Novel human arginine-rich US2004053250-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide WO200270539-A2. 12-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH18153 standard; cDNA; 1876 BP.
Human cDNA sequence SEQ ID NO:18038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human soft tissu WO2004048938-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ11562 standard; cDNA; 1897 BP.
Human polynucleotide SEQ ID NO 444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA
ABA04454 standard; cDNA; 1562 BP.
Human PP1187 protein encoding cDNA SEQ ID NO:10/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH08134 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-2004
                                                 (PETE/) PETERSON D P.
(PEAR/) PEARSON C I.
(COCK/) COCKS B G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                 (TANG/) TANG Y T.
                                                                                                                                                                                                                                                                                                                                                                                            DM44080 standard; cDNA; 1897
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                                                                                                                                                                                                                                           INC.
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SEQ ID NO:4969.
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No. 1.
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No. 3.
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No. 3.
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No. 3.
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No.
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No. 2.
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No. 3.7e-08;
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.7e-08;
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'.9e-10;
                              DB 10;
.7e-08;
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.7e-08;
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.7e-08;
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.5e-10;
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.6e-08;
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Best Local Similarity
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RESULT 202
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19-SEP-2001.
(SHAN-) SHANGHAI INST ONCOLOGY.
                                                                                                                                                                                                                                                                                            Tumour-associated WO2004030615-A2. 15-APR-2004.
                                                                                                                                                                                                         ADE54054 standard; cDNA; 2369 BP. Human prostate cancer cDNA #401. US2003190640-A1. 09-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                     ADK51980 standard; cDNA; 2277 Human atopic dermatitis/psoria WO2004016785-A1.
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(AUCK-) AUCKLAND UNISERVICES
21 Match 4.3%;
1t Local Similarity 59.7%;
                              US6607879-B1.
                                           Human cDNA
                                                     ADI30758 standard;
                                                                                                                                          ACC79092 standard;
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Tumour-associated antigenic target
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                                                                                                (INCY-)
                                                                                                         27-FEB-2003
                                                                                                                    WO2003016506-A2.
                                                                                                                           ACC79092 standard; cDNA;
Human secreted protein SI
                                                                                                                                                                                   (FARI/) FARIS M.
(PEAR/) PEARSON C
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                                                                        INCYTE GENOMICS INC. h 4.3%; Similarity 59.7%;
           INCYTE
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           CORP.
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59.7%;
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59.7%;
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                                                    CDNA; 1358
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Score 63.2;
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7 encoding
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Pred. No. 7.9e-07;
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.9e-07;
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.3e-07;
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Length 1358;
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RESULT 216
ID ABL498
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                                                                                                                                                                             ABL30333 standard; DNA; 1000 BP. Drosophila melanogaster genomic polynucleotide WO200171042-A2.
                                                                                                                  ABL49897 standard;
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Human PRO polynucleotide
US2004014039-A1.
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                   Intracellular calcium WO200210371-A1.
                                                                                                 Intracellular calcium ion transport WO200210371-A1.
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ry Match 4.2%;
t Local Similarity 60.0%;
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                                                                   (KYOW ) KYOWA HAKKO KOGYO KK.
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2/) RUBEN S M.
3/) BARASH S C.
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куома накко кодуо кк
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de SEQ ID N
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L human calcium-binding
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                                                                                                  AAK41013 standard; DNA; 186 Human bone marrow expressed WO200157276-A2.
                          Human brain expressed single WO200157275-A2.
                                                                                                                                                                         Probe #12389 for WC200157274-A2.
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Human foetal liver single ex
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                                             AAK15290 standard;
                                                               (MOLE-) MOLECULAR DYNAMICS
ry Match 3.7%;
t Local Similarity 72.9%;
                                                                                                                                                                                                                                        09-AUG-2001
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WO200157271-A2.
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Human breast cell single exc
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Probe #15752 used t
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MOLECULAR DYNAMICS INC.
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cimilarity 72.9%; Pred.
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RESULT 232
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                           Human bone marrow expressed WO200157276-A2.
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Probe #2629 used to
WO200157272-A2.
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Human liver single
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                                                                                                                                                                        Human breast cell single WO200157271-A2.
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(MOLE-) MOLECULAR DYNAMICS INC.
ty Match 3.7%; Score
72.9%; Pred.
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Human foetal liver
WO200157277-A2.
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(MOLE-) MOLECULAR DYNAMICS INC.
2.7%; Score
t Local Similarity 72.9%; Pred.
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ry Match 3.7%;
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Query Match
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RESULT 240
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RESULT 236
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                                                                                                 DNA homologous to phytopathogen W02003020905-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAI02500 standard;
Probe #2491 used to
WO200157270-A2.
                                      Plant DNA sequence WO2003020936-A1.
                                                                                                                                                                 DNA homologous to WO2003020905-A2.
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WO2003020905-A2.
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ry Match 3.7%;
t Local Similarity 72.9%;
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WO200157273-A2.
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Query Match
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RESULT 252
ID ADA71938
DE Rice gene
PN W02003000
PD 03-JAN-20
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ID ADK55;
DE Plant
PN WO200;
PD 13-MAI
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RESULT 245
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                                                                                         ADB52516 standard; DNA; 691 BP. Primary rat hepatocyte toxicity
                                                                                                                                                         Toxicity-related WO2003064624-A2.
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(DOWC ) DOW AGROSCIENCES LLC.

TYPE MAtch

TYPE Similarity 50.0%;
                                                                                                                                                                                                                                           ADK55190 standard; DNA; 6 plant DNA sequence which WO2003020936-A1.
                                                                                                                                                                                                                                                                           (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
ry Match
7.00al Similarity 50.0%;
                                                                                 WO2003065993-A2.
                                                                                                                                                                          ADB58040 standard; DNA;
                                                                                                                                                                                                                                                                                                                            ADK57006 standard; DNA; ePlant DNA sequence which WO2003020936-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               WO2003020936-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Plant DNA sequence which
                                                                                                                                                                                                                                                                                                                                                                                                                                ADK59086 standard; DNA; 620 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA homologous to phytopathogen resistance-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC77196 standard; DNA; 620 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC76480 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK55204 standard;
Plant DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                  (DOWC ) DOW CHEM CO.
                                                                                                                                       (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOWC ) DOW CHEM CO.
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                                                               GENE LOGIC
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                                                                                                                                                                  gene,
                                                    · INC.
                                                                                                                    C INC.
3.3%;
7 50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which
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50.0%;
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                                             3.3%;
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                                                                                                                                                                  ; 691 BP.
SEQ ID 3066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654
                                                                                                                                                                                                                                                             622 BP.
                                                                                                                                                                                                                                                                                                                                               620 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         654 BP.
                                                                                                                                                                                                                                                   confers altered metabolic
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                                                                                          modelling
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                                                                                                                                                                                                                                                                                                                                     altered metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          altered
                                                                                                                     49.2;
No. 0.
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No. 0.
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No. 0.
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No.
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No.
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No.
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No. 0.0048;
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No. 0.
                                           . 0.
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                                             DB 10;
.0066;
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.0048;
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Rice gene,

ADA71938 standard; DNA; 2000

ВÞ

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Query Match
Best Local S
RESULT 257
                                                                                      Best Local Similarity
RESULT 259
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                                                                                                          Query Match
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Best Local
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                                                                                                                                                                                                               AAC03907 standard; cDNA; Human secreted protein 5'
                                                                                                                                                                                                                                                                             Human His-tagged CN1412312-A.
                                                                                                                                                                                                                                                                                                                                                  Human secreted protein 5' EP1033401-A2.
                                                                                                                                                                                                                                                                                              ADL07540 standard;
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                                                      03-JAN-2003
                                                             WO2003000898-A1.
                                                                               ADA71938 standard;
                                                                                                                                  Human soft tissue
WO2004048938-A2.
                                                                                                                                                    ADQ23762 standard;
                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                      Human secreted EP1033401-A2.
                                                                                                                                                                                                                                         (CHON-) CHONGQING KANGERWEI 
ry Match 3.1%; 
t Local Similarity 51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prokaryotic essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA26827 standard; DNA; 2451
                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                     AAC01147 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS2004016025-A1.
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          DA58445 standard;
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                                                                                                                                                                    ocal Similarity
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PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                         GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                         SYNGENTA PARTICIPATIONS AG.
h 3.1%; Score
Similarity 9.9%; Pred. N
                                                                                                                 PROTEIN DESIGN LABS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
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3.3%; Score
                                                                       SEQ ID
synthase
                                                                                                                                                                                                                                                                                     Troponin
                                                                                                                                          sarcoma-upregulated
                                                                                                                                                                                                                                                                                     cDNA; 498 roponin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA; 768
                                                                                                                                                    DNA; 1001
                                                                                               3.1%;
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3.1%;
46.8%;
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51.5%;
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                                                                               2000
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          303
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 03 BP.
#89.
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Pred. No. 0.
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Pred.
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                           0.13;
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0.054;
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                                                                                                        Length 1001;
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17-JUL-2003

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Best
RESULT
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RESULT
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         Query Match
Best Local :
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                                                                                          Query Match
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                                                                                                               Human hyperpolarisation-activated W02002630-A2.
                                            Maize gene conferring WO2003000906-A2.
                                                                                                                                                                            02-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                               AAH98302 standard;
Human EST-derived o
WO200154477-A2.
                                                                                                                                                                                                                                                                                  Human tumour-associated WO2004060270-A2. 22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                      Human HCN2 cDNA. WO200159153-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Renal toxin progression WO2004048598-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxicity modell WO200295000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABT41999 standard;
Toxicity modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003.
(GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                         AAH48729 standard; cDNA; 3372 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP72640 standard; DNA; 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB58316 standard; DNA; 1112
                                                                ADA49154 standard;
                                                                                                                                                                                                                                                                                                              ADQ83419 standard; cDNA;
                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC INC.
3.0%;
TY Match 3.0%;
Local Similarity 49.8%;
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                           SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                    (SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                     AVET ) AVENTIS PHARMA DEUT
Local Similarity 269
                                                                                                                                                            Local Similarity
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                                                                           AE BEECHAM PLC.
3.0%; Score 4/
                                                                                                                                                                                                        ; cDNA; coding
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3.0%;
49.8%;
                                                                DNA; 447 BP.
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57.6%;
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                                                        disease
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d antigenic
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sequence
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         44.4;
No. 0.
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No. 0.
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0.12;
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0.12;
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0.12;
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.057;
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.28;
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.28;
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.28;
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.28;
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12;
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                                                                                                                                                                                                                                                                                                       #233
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Best Local Similarity
RESULT 271
ID ADDACCO
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Best Loca
RESULT 272
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                                                      Plant cDNA #3639.
US2004016025-A1.
22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ42631 standard; cDNA; 787 Plant cDNA #3631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA49026 standard; DNA;
                                                                                   ADJ42639 standard;
                                                                                                                                                                                                                                    US2004016025-A1.
                                                                                                                                                                                                                                                       ADJ42636 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KATA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003135888-A1.
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Wheat cDNA modulated by post-transcriptional
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                   COOP/
                            BRIG/)
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BRIGGS S.
COOPER B.
GLAZEBROOK J.
GOFF S. A.
KATAGIRI F.
KREPS J.
PROVART N.
BRICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                          BUDWORTH P.
MOUGHAMER T.
BRIGGS P.
COOPER B.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N.
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BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
                                                                                                                                                                                                                                                                                          RICKE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KATAGIRI F.
KREPS J.
                                                                                                                                                                                                       BUDWORTH P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZHU T. WANG X.
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RICKE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUGHAMER T.
PROVART N.
                                                                                                                                                                                                                                              #3636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.0%;
                                                                                   cDNA; 841
                                                                                                                                                                                                                                                       CDNA;
                                                                                                    3.0%;
                                                                                                                                                                                                                                                                       3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
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Pred. No. 0
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 0.15;
                                                                                                                                                                                                                                                                         No. 0.
                                                                                                     44.4;
No. 0.
                                                                                                                                                                                                                                                                         4; DB
0.15;
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.15;
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.15;
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                                                                                                               12;
                                                                                                                                                                                                                                                                                   12;
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                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               silencing SeqID
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B R R G
Best Local Similarity 49.2*; Pred. No. 0.33;
RESULT 282
ID AAS44950 standard; cDNA; 2247 BP.
DE cDNA encoding novel human secretory protein, Seq ID No
                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                         SABI
                                                                                                    RESULT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 274
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                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                      Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian specific gene s
WO2004013311-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN83907 standard;
Calcium sensor G85
EP1209167-A1.
                                                                                                                                                             ABD21000 standard; DNA; 2190 Human calmodulin 2 DNA.
                                                                                ADN60285 standard;
Human calmodulin 2
                                                                                                                                                                                                                            WO200285308-A2.
31-OCT-2002.
                                                                                                                                                                                                                                            ABZ84770 standard; DNA; 2190
Human calmodulin 2 gene.
                                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC INC.
3.0%;
ry Match
- romal Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                             Human cDNA differentially expressed in
                                                                                                                                                                                                                                                                                                                                       ABK83767 standard; cDNA; 2175 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian specific gene WO2004013311-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ67515 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC40960 standard; DNA;
                                                                                                           (EPIG-) EPIGENESIS PHARM INC.
ry Match 3.0%;
t Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                   VO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2002.
(OKAZ-) OKAZAKI NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZHUT/)
                                                                                                                                                                                                                EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                DIAD-) DIADEXUS INC.
                                                                                                                                                                                            ocal Similarity
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PROVART N.
RICKE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZHU T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 1251
encoding s
                                                                              cDNA; 2190 BP.
encoding cDNA.
                             1 INC.
3.0%;
49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 1527
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3.0%; ;
49.2%; ;
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49.2%;
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SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
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D NO: 30145
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Pred.
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Pred. No. 0.16;
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No.
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No.
                                                                                                              DB 11;
0.33;
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0.27;
                               DB 13;
0.33;
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0.33;
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0.25;
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0.16;
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0.27;
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Query Match
Best Local S
RESULT 283
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Best Local Similarity
RESULT 288
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RESULT 286
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Best Local Similarity
RESULT 284
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                                                                                                                                                                                                                                                                                                                                             ABL63305 standard; DNA; 1161 Breast cancer related gene se WO200194629-A2.
                                                                                      ADT66612 standard;
Rat calmodulin cDNA
                                                                                                                                                          AAX90998 standard; DNA; 6710
Human centrin-2 genomic seque
WO9951186-A2.
14-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ84750 standard; cDNA; 2363 BP. Human tumour-associated antigenic W02004060270-A2.
AAC55847 standard; DNA; Mitomycin biosynthetic gW0200053737-A2.
                                                                                                                                                                                                                                                                Human centrin-2 gene WO9951186-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA58674 standard; cDNA; 255 BP.
Maize sucrose synthase EST #318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ86930 standard; cDNA; 2363 BP. Human tumour-associated antigenic WO2004060270-A2.
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                                                                             WO2004070383-A2.
                                                                                                                                       (MILL-) MILLENNIUM PHARM INC (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003135870-A1.
                                                           (CHEF ) GRUENENTHAL
                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                         AAX90997 standard; DNA; 1173 B
Human centrin-2 gene (Hcen-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH (WUTD/) WU T D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                            (AVAL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH (WUTD/) WU T D.
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                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                       CDNA.
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                                                                                                 CDNA; 1084
                                                                                                                                                                                                                                                                                                       2.9%;
52.8%;
                                     . GMBH.
2.9%;
49.3%;
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       ; 2466
gene c
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         cluster
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Pred.
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                                      43.4;
No. 0.
                                                                                                                    No.
                                                                                                                                                                                                             43.6; DB
No. 0.31;
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No. 0.
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No.
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         related
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0.34;
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0.34;
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.31;
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.13;
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.34;
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        alpha
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         amylase orf20
                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence #3805.
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Query Match
Best Local S
RESULT 297
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RESULT
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                                                          ADO21558 standard; DNA; 450 BP. Calmodulin mutant Y99F/Y138F-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE10328 standard;
S. lavendulae gene
US2003134398-A1.
                                                 WO2004046179-A1.
                                                                                                                              EP1209167-A1.
                                                                                                                                      ABN83905 standard; cDNA; 447 BP. Rat calmodulin encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC55841 standard;
Complete Mitomycin
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17-JUL-2003.
                                                                                                                                                                                                                                       Maize sucrose synthase
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                                                                                                                                                                                     (CHBI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                             JS2003135870-A1.
                                                                                                                                                                                                                                                ADA58464 standard;
                                                                                                                                                                                                                                                                                                                                                                   ADE10260 standard; DNA;
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(MAOY/) MAO Y.
(VARO/) VAROGLU M.
                              CNSJ )
                                                                                                                                                                                                                                                                                                                                                                                                         SHEL/) SHELDON P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMM/) HE M.
SHEL/) SHELDON P.
                                                                                                          OKAZ-) OKAZAKI NAT
                                                                                                                                                                                                                                                                                                 HEMM/) HE M.
                                                                                                                                                                                                                                                                                                                            SHER/) SHERMAN D H.
  Local Similarity
                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                   ocal Similarity
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HE M.
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SHERMAN D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SHERMAN D H. MAO Y.
                                                                                                                                                                                                                                                                                                                    MAO Y
                                                                                                                                                                                                                                                                                       SHELDON P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV MINNESOTA.
            CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

n 2.9%; Score 43.2; DB 12;
Similarity 50.5%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                        VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                             VAROGLU M.
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for orf20.
                                                                                                                                                                                                                                                  cDNA;
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ORF 11-22 1
                                                                                       RES INST.
2.9%;
50.5%;
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                                                                                                                                                                                                                                        A; 294 BP.
EST #108.
                                                                                                                                                                                                                                                                                                                                                          18034 BP.
C gene cluster
                                                                                                                                                                                                                                                                                                                                                         gene
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Pred.
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Pred.
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Pred.
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Pred. No. 1
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No. 0.
                                                                                         43.2;
No. 0
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No. 0.
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No. 1
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..4;
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                      Length 450;
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Query Match
Best Local S
RESULT 305
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RESULT 304
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RESULT 303
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RESULT 302
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Best Local
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Best Local Similarity
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18-SEP-2003.
(NEUR-) NEUROGENEX CO LTD.
2:9%;
2ry Match 2:9%;
50:5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EP1033401-A2.
AAA31901 standard; DNA; 495
Plant microsatellite marker
WO9967421-A1.
29-DEC-1999.
(GENE-) GENESIS RES & DEV CO
                                                                                                                                                                                                                                   Plant microsatellite WO9967421-A1.
                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT 2.9%; Y Match 2.9%; 54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD45852 standard; cDNA; 2908 BP.
Corn sucrose synthase (Sus1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF60791 standard;
BCC DNA #SEQ ID 13.
WO2003076466-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO21556 standard; DNA; 450 BP. Calmodulin mutant Y138F-encoding DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calmodulin mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC03838 standard; cDNA;
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                                                                   (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FOREST I TY Match 2.9%; Score t Local Similarity 48.9%; Pred.
                                                                                                                            WO9967421-A1.
                                                                                                                                          AAA31434 standard; DNA; 450
Plant microsatellite marker
                                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                                                                           AAA31581 standard;
                                                                                                                                                                                                                                                                                                      (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                     Maize sucrose sy
US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                            ADA58522 standard;
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                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD (FLET-) FLETCHER CHALLENGE FOREST 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONSEJO SUPERIOR INVESTIGACIONES h 2.9%; Score 43.2; Similarity 50.5%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID 13.
                                                                                                                                                                                                                                                                                                                                                                 synthase
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Y99F-encoding DNA,
                                                                                                                                                                                                                                                DNA; 378
te marker
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nase EST #166.
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#862.
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#395.
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#542.
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Pred.
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Pred. No.
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Pred.
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No. 0
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0.23;
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0.26;
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DB 12;
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Query Match
Best Local S
RESULT 312
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ID ADC759
DE DNA hc
PN WO2003
PD 13-MAR
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                                                                                                                                                                       ADC75909 standard; DNA; 624 BP. DNA homologous to phytopathogen resistance-related w02003020905-A2.
                                                                                                                                                                                                                                            DNA homologous to WO2003020905-A2.
                                   ADK56990 standard;
Plant DNA sequence
                                                                          (DOWC ) DOW AGROSCIENCES LLC.
                                                                                                             ADK59089 standard; DNA; 624 BP.
Plant DNA sequence which confers altered
                                                                                                                                                                                                                                                             ADC77180 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     ADA58468 standard; cDNA;
Maize sucrose synthase E:
US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ42635 standard;
Plant cDNA #3635.
                          WO2003020936-A1.
                                                                                                       #O2003020936-A1.
                                                                                                                                                                                                                                                                                                                                  US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                          Maize sucrose synthase EST #99.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FLET-) FLETCHER
                                                                                                                                                                                                                                                                                                (LIUJ/) LIU J.
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                                                                                                                                                       DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                   DA58455 standard;
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FISH/) FISHER D K.
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                                                          Local Similarity
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ZHU T.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                          DOW CHEM CO
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PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLAZEBROOK J.
                                  ведчепсе
CHEM CO.
AGROSCIENCES LLC.
                                                                                     CHEM CO
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2.9%; Score 43;
ty 48.9%; Pred. No.
                                                                                                                                                                                                                                                    ; DNA; 624 BP.
phytopathogen
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                                 DNA; 624 BP. which confers
                                                                                                                                                                                                                                                                                                                                                   CDNA; 313 BP
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                                                          2.9%;
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EST #112.
                                                          Score
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                                  altered
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No. 0.
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No. 0.
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No. 0.
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No. 0.
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.43;
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.43;
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.31;
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                                  metabolic
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                                  characteristic #4373
                                                                                                              characteristic #6472.
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Query Match
Best Local S
RESULT 321
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RESULT 315
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RESULT 319
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RESULT 317
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RESULT 314
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                                                                                                                                                                    ABI99274 standard; cDNA; 1361 BP. Mouse ischaemic condition related W0200188188-A2.
                                                                                                                                                                                                                                                                                                         (DOWC ) DOW CHEM CU.
(DOWC ) DOW AGROSCIENCES LLC.
(DOWC ) DOW AGROSCIENCES LLC.
2.8;
2.9; Match 48.24;
         AAH74541 standard; cDNA;
Nucleotide sequence of a
                                                                                             ADT66614 standard;
Murine calmodulin o
                                                                                                                                                                                                                                      (DOWC )
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Plant DNA sequence which
WO2003020936-A1.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                   ADK56997 standard; DNA; 695 BP. Plant DNA sequence which confers altered metabolic WO2003020936-A1.
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WO2004060304-A2.
Nucleotide sequence WO200146387-A1.
                                                                         19-AUG-2004.
                                                                                                                          (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON ry Match 2.8%; Score 41.8; 1 Local Similarity 48.9%; Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA homologous two2003020905-A2.
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WO2003020905-A2.
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                                                               (CHEF ) GRUENENTHAL
                                                                                   WO2004070383-A2.
                                                                                                                                                            22-NOV-200
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(DOWC ) DOW AGROSCIENCES LLC.
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ry Match 2.8%;
t Local Similarity 47.7%;
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                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 674 BP. sequence which confers altered metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ndard; DNA, 28516 BP.
associated sequence
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                                                                                             ; cDNA; 1361 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                       . GMBH.
2.8%;
48.9%;
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h confers altered metabolic
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         905 BP.
chitobiosidase
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Pred.
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Pred. No. 0.
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                                                                                                                            11.8; DB
No. 1.1;
                                        41.8;
No. 1.
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No. 0.
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No. 0.
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No. 0.
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No. 0.
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No. 0.
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                                                                                                                                                                               sequence
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4.3,
                                     DB (.1)
       polypeptide
                                                                                                                                                                                                               DB
.76;
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.76;
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.75;
                                                                                                                                                                                                                                                                                                             DB
.76;
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.76;
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.43;
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                                                                                                                                                                                 SEQ
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                                                                                                                                     Length 1361;
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                                                   1361;
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Best Local Similarity
RESULT 322
ID ADA49171
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Best Loca
RESULT 325
                                                                                                                                                                                                                          RESULT
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA49171 standard; DNA; 447 BP. Maize gene conferring disease r WO2003000906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ12052 standard; DN Maize cDNA modulated US2003135888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUN-2001.
(CORR ) CORNELL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2003.
(ZHUT/) ZHU T.
(WANG/) WANG X.
(CHAN/) CHANG H.
                                                                                                                                                                                                                                                                          (BUDW/) BUDWORTH P.
(MOUG/) MOUGHAMER T.
(BRIG/) BRIGGS S P.
(COOP/) COOPER B.
                           DNA, 521 BP.
DNA homologous to phytopathogen resistance-related WO2003020905-A2.
                                                                               DNA homologous to phytopathogen WC200320905-A2.
WC20033.
13-MAR-2003.
(DOWC ) DOW CHEM CO.
                                                                                                                                                                ADQ97220 standard; DNA; 52640 BP.
Mouse cancer associated sequence MD08-015,
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                          ADJ42640 standard;
Plant cDNA #3640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA PARTICIPATIONS AG

CY Match

Local Similarity

51.1%; Pred.
                                                                                                                                                                                                                                                                                                                   US2004016025-A1.
                                                                                                                 ADC76479 standard; DNA; 521 BP.
                                                                                                                                  (SAGR-) SAGRES DISCOVERY INC.
ry Match
Local Similarity 57.9%;
                        L3-MAR-2003
                                                                ocal Similarity
                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                    cal Similarity
                                                                                                                                                                                                                                                                                                                                                                  GOFF S A.

KATAGIRI F.

KREPS J.

MOUGHAMER T.

PROVART N.

RICKE D.
                                                                                                                                                                                                                  RICKE D.
                                                                                                                                                                                                                                  KATAGIRI F.
KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                    GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                             BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                          GLAZEBROOK J.
GOFF S A.
                DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S FOUND IN
2.8%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                                                                                   2.8%;
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                                                                 2.8%;
2.8%;
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                                                                                                                                                                                                                                                                                                                                      727
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Pred.
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Pred.
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Pred.
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                                                                 Score
Pred.
                                                                                                                                                                                                   Score 41.2;
Pred. No. 1.
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Score
Pred.
                                                                                                           resistance-related
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No. 0.
                                                                                                                                                                                                                                                                                                                                                      41.2;
No. 0
                                                                  NO.
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1
 41;
No.
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                                                                  1.1;
  DB
1.1;
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..1;
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(.7;
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                                                                                                                                                                            SEQ
                                                                         10;
         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                          Length 52640;
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                                           cDNA
                                                                                                             CDNA -
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                                           日
                                                                                                              1748
                                           2122
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Local Similarity

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RESULT 328
ID ADK570
DE Plant
PN WO2003
PD 13-MAF
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ID AD
DE P1
PN WO
PD 13
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Best Local S
RESULT 334
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                                                                                                      Best Local Similarity RESULT 335
                  Best Loc
RESULT 336
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Best Local
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                                    Query Match
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Plant DNA sequence v
WC2003020936-A1.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant DNA sequence
WC2003020936-A1.
13-MAR-2003.
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(DOWC ) DOW AGROSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                 AAC43155 standard; DNA;
Arabidopsis thaliana DNA
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ51912 standard; cDNA; 936 BP.
Aspergillus oryzae polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK55199 standard;
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WO200279476-A1.
                                                                                                                                                                                                                                          Arabidopsis tha WO200281695-A2.
                                                                                                                                                                                                                                                                                                                                                   ABZ14388 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NORQ ) NAT FOOD RES INST MIN AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NAAD-) NAT INST ADVANCED (NARE-) NAT RES INST BREWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DOWC ) DOW AGROSCIENCES
                                                                                                            03-JAN-2003.
03-JAN-2003.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA PARTICIPATIONS

TY Match
2.8%; Scc
Local Similarity 48.9%; Pre
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
WO200216655-A2.
                                                                        Aspergillus oryzae
WO200056762-A2.
                                                                                           AAF14569 standard;
                                                                                                                                                      Arabidopsis thal
WO2003000898-A1.
                                                                                                                                                                          ADA68286 standard; DNA;
                                                                                                                                                                                                                                                      ABZ42072 standard; cDNA; 975 E
Arabidopsis thaliana gene #56
                                                                                                                                                                                                            (SYGN ) SYNGENTA PARTICIPATIONS (FRIE-) FRIEDRICH MIESCHER INST.
Human
ADJ67514 standard; DNA;
Human ovarian specific (
                                              NOVO ) NOVO
                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
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                                              NORDISK AS.
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which
                                                                                    cDNA; 1129
EST SEQ ID
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48.5%;
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48.5%;
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                            2.8%;
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h confers altered
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h confers altered metabolic characteristic #4386.
 ; 1457
gene s
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A fragment SEQ
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Pred.
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6 modulated
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Pred.
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NO:7092.
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                                                                                                                                                                   847.
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No.
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No.
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No.
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No.
   NO:228.
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1.1;
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1.1;
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1.5;
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                               DB
1.6;
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1.5;
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Best Loca
RESULT 337
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WO2004013311-A2
12-FER-200
                                                                                             Murine cancer-associated WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                        AAQ04334 standard; DNA; 504 plasmid pOCAL7 contg. gene JP02092286-A.
                                     Bovine embryonic germ
                                               ABN74463 standard;
                                                                                                    ABD33266 standard; DNA; 168407 BP.
Murine cancer-associated (CA) gene
                                                                                                                                                                                                                                                   ADJ41936 standard; cDNA;
Plant cDNA #2936.
                                                                                                                                                                                                                                                                                                                          Cotton cDNA sequence, US2004181830-A1.
                                                                                                                                                                                                                                                                                                                                         ADR64131 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant calmodulin JP02092286-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ04331 standard; cDNA; 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004013311-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       (KIRI ) KIRIN BREWERY KK.

ry Match 2.7%;
t Local Similarity 49.8%;
                                                                                                                                                                                                                                           JS2004016025-A1.
                                                                                                                                                                                                                                                                                          (KOVA/) KOVALIC D
(ZHOU/) ZHOU Y.
(CAOY/) CAO Y.
                                                                                                                                                                                                                                                                                                                                                        (KIRI ) KIRIN BREWERY KK.

CY Match

Local Similarity 49.8%;
                                                                              SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                  -APR-1990
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                                                               ocal Similarity
                                                                                                                                                                                                                                                                           ocal Similarity
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                                                                                                                                                                                                    BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                    KREPS J.
PROVART N.
RICKE D.
Similarity
                                                                                                                                              ZHU T.
                                                                                                                                                                           GOFF S A.
KATAGIRI F.
                                                                                                                                                                                   GLAZEBROOK J.
GOFF S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INC.
                                      cDNA; 974 BP.
erm (EG) cell
                                                              2.7%;
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2.7%;
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4912
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Pred.
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Pred.
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                                                                                                    gene
                                       CDNA
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40.4; DB
No. 2.2;
                                                               40.6;
No. 25;
                                                                                                                             40.6;
No. 1.
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No. 1.
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No. 1.
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No. 2.
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No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                447;
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Best
RESULT
Best Local Similarity
                                                                                                                                                                                                                      Best Loca
RESULT 350
                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 349
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                                                                                                                                             RESULT 351
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                                                                                                                                                                                                                                       Query Match
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                                  ADB53373 standard; DNA; 3513 BP. Primary rat hepatocyre toxicity WO2003065993-A2.
14-AUG-2003.
                                                                                                                          ADB58685 standard; DNA; 3513 I
                                                                                                                                                                                                    ADQ22652 standard; DNA; 3446
Human soft tissue sarcoma-upr
                                                                                                                                                                                                                                                                           ACA43874 standard; DNA; 2394
Prokaryotic essential gene #:
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Bovine embryonic germ (EC
WO200194550-A2.
                                                                                                                  WO2003064624-A2.
                                                                                                                                                                                           WO2004048938-A2.
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2.7%; Sc
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(FISH/) FISHER I
(LIUJ/) LIU J.
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Toxicity modelling
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WO2003020905-A2.
                                                                                       AAA31443 standard; DNA; 350 Plant microsatellite marker
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ry Match 2.7%;
t Local Similarity 47.3%;
                  ADC77194 standard;
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                                                      (GENE-) GENESIS RES & DEV CORP LTD.
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13-MAR-2003.
(10WC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
(DOWC ) TOWN AGROSCIENCES LLC.
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Toxicity modelling
WO200295000-A2.
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Rice gene, SEQ ID :
WO2003000898-A1.
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it Local Similarity 50.3%; Pred.
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Plant DNA sequence
ADS55071 standard; cDNA; Bacterial polynucleotide US2003233675-A1.
                                                                                    Rice gene, SEQ I
WO2003000898-A1.
                                                                                              ADA69683 standard; DNA; 1248 Rice gene, SEQ ID 3006.
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2.7%;

ry Match 2.7%;

t Local Similarity 48.9%;
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                                          (SYGN ) SYNGENTA PARTICIPATIONS AG
ry Match 2.7%; Score
t Local Similarity 50.3%; Pred.
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(GENE-) GENE LOGIC
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sequence which confers altered
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2.7%;
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                           ADJ41937 standard; cDNA; Plant cDNA #2937.
                                                                                                                       ADA48926 standard; DNA; 709 BP. Wheat gene conferring disease r
                                                                                                                                                                                                                                                                   Plant cDNA #3634.
                                                                                                                                                                                                                                                                                                                               AAN80188 standard; DNA; 46
DNA encoding biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                    Mouse ischaemic
WO200188188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial polynucleotide US2003233675-A1.
                                                    US2004016025-A1.
                                                                                                                                                                                                                                                                         ADJ42634 standard;
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                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS AG.
TY Match 2.7%; Score
Local Similarity 49.1%; Pred.
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                           BUDWORTH P.
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ZHU T.
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CHEN X.
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BRIGGS S P.
COOPER B.
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BUDWORTH P.
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PROVART N.
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KATAGIRI F.
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2.7%; (
Similarity 48.3%; )
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                                                ABN80303 standard; DNA; 6120 BP. Human chemically modified disease WO200200927-A2.
                                                                                                                                                                                    ABN80332 standard; DNA; 3001 BP. Human chemically modified disease associated WO20020927-A2.
                                                                                                                                                                                                                                                        Rice gene, SEQ II
WO2003000898-A1.
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                                                                                                                   DNA transcription WO200192565-A2.
                                                                                                                                   ABK28440 standard;
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                                                                                                                                                                                                                                                                ADA69549 standard; DNA; 1434 Rice gene, SEQ ID 2872.
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ry Match 2.7%;
Local Similarity 48.3%;
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standard; DNA; 118063 BP
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                                                                     ADA70926 standard; DNA; 1146
Rice gene, SEQ ID 4249.
WO2003000898-A1.
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                                                                                                                                     AAC50296 standard; DNA; 514 BP. Arabidopsis thallana DNA fragment EP1033405-A2.
06-SEP-2000.
                                                                                                                                                                                                                                        Murine carcinoma associated (CA) US2004072154-A1.
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       ADJ40264 standard;
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(FIVE-) FIVE PRIME THERAPEUTICS INC.
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ry Match 2.7%; Score 39.4; D
t Local Similarity 45.8%; Pred. No. 7.9;
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ry Match 2.7%;
t Local Similarity 48.4%;
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(ENGE/) ENGELHARD E
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Human cardiac troponin C
W09739132-A1.
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Human adult heart cDNA #2768
US2003073623-A1.
17-APR-2003.
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17-APR-2003.
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Human adult heart cDNA #1029.
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(COOP/)
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                                                                                                                                                                              (DICK/) DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                         DRMA/) DRMANAC R T.
LABA/) LABAT I.
                                                                                                                                                                                                                                                                                                           DRMA/) DRMANAC R T.
LABA/) LABAT I.
STAC/) STACHE-CRAIN
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GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RICKE D.
ZHU T.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                   SPECTRAL DIAGNOSTICS
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standard; cDNA; 795
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Best Local Similarity
RESULT 402
ID ACH03848 standard; c
DE Human CDNA different
PN US2003065157-A1.
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Best Loca
RESULT 407
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Best Local
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18-SEP-2003.
(SHIQ/) SHI Q.
(SONG/) SONG Q.
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05-NOV-2002.
(SPEC-) SPECTRA
                                                                                                                                                                                                                                                                                                                                                  18-SEP-2003.
(SHIQ/) SHI Q.
(SONG/) SONG Q.
                      ADQ23279 standard; DNA; 1225
Human soft tissue sarcoma-upr
WO2004049938-A2.
10-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE77154 standard; cDNA; 846 BP. Human cDNA differentially expressed US2003108871-A1.
                                                                                                                                                                    Human cardiac WO9931235-A1.
                                                                                                                                                                                                                                   ADE77155 standard; cDNA; 1158 Human cDNA differentially expr
                                                                                                             Human cDNA encoding
                                                                                                                      ADG14205 standard;
                                                                                                                                    (SPEC-) SPECTRAL DIAGNOSTICS 2.6%; Local Similarity 51.4%;
                                                                                                                                                                            AAX78382 standard; DNA; 1173
Human cardiac troponin I and
                                                                                                                                                                                                                                                                                                            DNA encoding cardiac troponin
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                                                                                                                                                                                                                                                                                                                                                                                           ADG14210 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACH03848 standard; cDNA; 844 BP
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                (PROT-)
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                PROTEIN DESIGN LABS
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RESULT 417
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RESULT 414
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RESULT 413
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         Query Match
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17-SEP-1998.
(REGC) UNIV CALIFORNIA.
2-6%;
Arv Match 2-6%;
48.8%;
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Parapoxvirus ovis genome DNA seque
2:6%; Score
3: Match 50.3%; Pred.
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2:ry Match
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48.8%;
                                                AAA31857 standard; DNA; 278 Plant microsatellite marker WO9967421-A1.
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Human immune system associated c
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(REGC ) UNIV
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26-SEP-2002.
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Human activated T cell cDNA #1
                 (GENE-) GENESIS F
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th 2.6%;
Similarity 48.8%;
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HAWKINS P R.
                             GENESIS RES
 CHALLENGE FOREST LTD.

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ty 47.9%; Pred. No.
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               Human cDNA diffe
US2002160382-A1.
31-OCT-2002.
                                ADA10931 standard; cDNA; ?
Human cDNA differentially
                                                                                         Bacterial source DNA WO2004033668-A2.
                                                                                                         ADM99174 standard;
                                                                                                                                                                  Human zygote arrest WO2003091400-A2.
                                                                                                                                                                                                                                   Lung carcinoma WO200107611-A2.
                                                                                                                                                                                                                                          AAF93577 standard; c
                                                                                                                                                                                                                                                                                                   Mouse mitochondrial WO2003020220-A2.
                                                                                                                                                                                                                                                                                                                                                                                   Human genome derived US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA69781 standard; DNA; 1650 Rice gene, SEQ ID 3104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200295000-A2.
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Toxicity modelling
                                                                                                                                                                                   ADJ63193 standard;
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                                                                                                                                                                                                                                                                                                                                                  (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                     ACH89551 standard;
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ry Match 2.6%; Score
L Local Similarity 50.0%; Pred.
                                                                                                                                        (BAYU ) BAYLOR (AMHP ) WYETH.
                                                                         DIVE-) DIVERSA CORP.
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JONES D
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Similarity 48.4%;
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48.4%;
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Human therapeutic I
WO2004080148-A2.
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Renal cell carcinon
                                    Human cDNA encod
US2003073196-A1.
                                            ADA43552 standard; cDNA; 2945 BP.
Human cDNA encoding secreted/transmembrane
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                          ADB99827 standard; cDNA;
Human PRO polynucleotide
US2003073192-A1.
17-APR-2003.
                                                                                                      ADB66149 standard; cDNA; 2945 BP. Human cDNA encoding secreted/transmembrane US2003082729-A1.
                                                                                                                                                                         ADB86994 standard; cDNA;
Human PRO polynucleotide
US2003082726-A1.
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Human PRO polynucleotide SEQ J
US2003082728-A1.
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10-APR-2003.
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Novel human secreted and
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US2003068780-A1.
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                                                                                                            ADD95483 standard; cDNA; 2945 BP.
Human cDNA encoding secreted/transmembrane
US2003064473-A1.
03-APR-2003.
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Human PRO28700 cDN/
US2003073194-A1.
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ADE38188 standard; cDNA; 2945 BP.
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Human PRO polynucleotide #44.
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US2003077741-A1.
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                                                                       Human cDNA encoding secreted/transmembrane US2003104561-A1.
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Human PRO polynucleotide #44.
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Human PRO polynucleotide #44.
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Human cDNA encoding secreted/transmembrane US2003073188-A1.
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         ADE37712 standard;
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Human PRO polynucleotide #44.
US2003138896-A1.
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Human PRO polynucleotide #44.
US2003096364-A1.
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Human PRO polynucleotide #44.
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Human PRO polynucleotide
US2003119117-A1.
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US2003124666-A1
                                                           (GETH ) GENENTECH INC.
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DE Human cDNA encoding
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        Human cDNA encoding US2003104563-A1.
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Human PRO polynucleotide #44.
US2003124663-A1.
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Human PRO polynucleotide #44.
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Human PRO28700 cDN/
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                                           Human cDNA encoding US2003119136-A1.
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Novel human secreted and
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                           ADI13596 standard; cDNA; Novel human secreted and US2003119131-A1.
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Novel human secreted and
US2003119128-A1.
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          (FISH/)
(LIUJ/)
                                                                                                                                                                                                    ACN45200 standard; DNA; Mouse genomic sequence mWO2003073826-A2.
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Human zygote arrest 1 (Zar1)
W02003091400-A2.
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                                              Maize sucrose synthase US2003135870-A1.
                                                                                                                        Human secreted EP1033401-A2.
                                                                                                                                 AAC23266 standard; cDNA; 214 BP.
Human secreted protein 5' EST, SEQ
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ry Match
2.6%;
Local Similarity 58.1%;
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Human cDNA encoding secreted/transmembrane
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(FISH/) FISHER D I
(LIUJ/) LIU J.
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ADA58895 standard; cDNA; 383
                                       (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                         ADA58904 standard; cDNA; 360 BP.
Maize sucrose synthase EST #548.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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(FISH/) FISHER D K.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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#136.
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#179.
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Pred.
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Pred. No. 4
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                     38.4;
No. 4.
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No. 4.
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No. 4.3;
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No. 4
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No. 4
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4.5;
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                                                                                                                                                                                                                                    Length 306;
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                              Length
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Query Match
Best Local S
RESULT 537
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RESULT 538
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Best Local Similarity
RESULT 535
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Best Local Similarity
RESULT 540
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        Query Match
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17.JUL-2003.
(CHBI/) CHEIKH N.
(FISH/) FISHER D F
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                             ADA58909 standard; cDNA; 413
Maize sucrose synthase EST #5
US2003135870-A1.
17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize sucrose synthase
                                                                                                                        ABN95419 standard;
Gene #1917 used to
WO200229103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant cDNA #2964.
US2004016025-A1.
                 ADA03007 standard; cDNA; 450 BP.
Mouse Calm2 carcinoma associated
W02003057146-A2.
17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                   ADA58893 standard; cDNA;
Maize sucrose synthase ES
US2003135870-A1.
17-JUL-2003.
                                                                                                                                                                                                                                                                                         (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
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US2003135870-A1. 
17-JUL-2003.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                     (GENE-) GENE LOGIC
Local Similarity
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KREPS J.
PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
                                                                                                                                                                                                                                                                                                                                             synthase EST
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                                                                               2.6%;
2.6%;
52.9%;
                                                                                                                                  DNA; 442
diagnose
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lase EST #519.
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 49.0%;
                                                                                                                                                                                                                                          IA; 433 BP.
EST #537.
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          2.6%;
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#553.
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liver cancer.
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Pred.
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  Score 38.4;
Pred. No. 5.
                                                   coding sequence,
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No. 5.
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No. 5.
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3.2;
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           Length
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                                                      SEQ ID NO:1525
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ADB72745

CDNA;

450

ВP

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Best Local Similarity
RESULT 549
ID ADK56992 standard; D
DE Plant DNA sequence w
PN W02003020936-A1.
PD 13-MAR-2003.
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Best L
                                                Query Match
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                                                                               ADC75913 standard; DNA; 595 BP.
DNA homologous to phytopathogen resistance-related
                                                                                                                                          DNA homologous to WO2003020905-A2.
                                                                                                                                                          ADC77182 standard;
                                                                                                                                                                                                         Human ovarian antigen WO200200677-A1.
                                                                                                                                                                                                                           ABQ55780 standard;
                                                                                                                                                                                                                                                                                             Maize sucrose synthase
US2003135870-A1.
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Mouse Calm2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                              ADA58866 standard; cDNA;
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(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC85487 standard;
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                                                                                                                                                                                           (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                           (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                             (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                             DA58877 standard; cDNA;
                                                        DOWC ) DOW CHEM CO
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                                                                                                         ocal Similarity
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2.6%;
Similarity 49.0%;
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                                                                                                                                                 ; DNA; 595 BP. phytopathogen resistance-related
                which
                        DNA;
                                                                                                                                                                                                                   cDNA; 591 |
gen HOPKG47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                         SCI INC.
2.6%;
49.3%;
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EST #521.
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                confers altered
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              metabolic characteristic #4375.
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Query Match
Best Local S
RESULT 550
         RESULT 558
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RESULT 555
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AAA27845 standard; cDNA; 916 BP.
AAA27845 standard; cDNA.
Soybean calmodulin-5 cDNA.
1 EP101853-A1.
D 12-JUL-2000.
A (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
A (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
2.6%; Score 38.4; D'
47.8%; Pred. No. 7.8;
                                                                                                                                   Query Match
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16-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
2:5%;
2:ry Match 2:5%;
52:5%;
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ADA58496 standard; cDNA; 288
                                                                                Maize sucrose sy US2003135870-A1.
                                                                                                                       (SAGR-) SAGRES DISCOVERY.

ry Match 2.6%;
t Local Similarity 42.1%;
                                                                                                                                                                  MO2003073826-A2.
                                                                                                                                                                            ACN44740 standard; DNA; 101241 BP. Mouse genomic sequence mCG3043.
                                                                                                                                                                                                                                                  Human genomic se
WO2003073826-A2.
                                                                                                                                                                                                                                                            ACN45034 standard; DNA; 99588 BP. Human genomic sequence hCG1640838
                                                                                                                                                                                                                                                                                                                                     Human nervous system WO200159063-A2.
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Human nervous system related
                                       (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                      ADA58523 standard; cDNA;
                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                         ABA16488 standard;
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                   Similarity
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DOW AGROSCIENCES
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                                                                                          synthase
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em related
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48.6%;
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48.6%;
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                                                                                          281 BP.
ST #167.
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No. 18;
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No. 6.3;
                    38.2;
No. 4
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No. 8
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No. 6.
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                          RESULT 565
                                                                                            Best Local Similarity RESULT 564
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                                                                                                                                                                                                                                                                    Query Match
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US2003135870-A1.
ADS49594 standard; cDNA; 2313 BP. Bacterial polynucleotide #4337. US2003233675-A1.
                                                                                                                                                                                                                         ADJ42633 standard;
Plant cDNA #3633.
US2004016025-A1.
                                                                                                                                                                                                                                                                                             ADE07673 standard; DNA; 747 BP. Novel coding sequence (useful f WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                                                                        ACH87297 standard; DNA; 603
Human genome derived single
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC41022 standard; DNA; 388 BP. Zea mays DNA fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize sucrose synthase US2003135870-A1.
                                                                                    AAQ99367 standard;
                                                                                                                                                                                                                                                                                                                                                                                US2003194704-A1.
                                                  (CANG-) CANGENE CORP.
                                                                                                                                                                                (MOUG/)
(BRIG/)
(COOP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHEI/) CHEIKH N.
(FISH/) FISHER D
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHBI/) CHBIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                             PENN/) PENN S G.
RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                           HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                 Local Similarity
                                                                          lividans protease
                                                                                                                                                                                                                                                            ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                      GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                      KREPS J.
PROVART N.
                                                                                                                     ZHU T.
                                                                                                                              RICKE D.
                                                                           DNA; 179
                                                                                                                                                                                                                                            cDNA; 800
                                                                                                                                                                                                                                                                                                                                                                                                                  2.6%;
                                2.6%;
                                                                                                                                                                                                                                                           2.6%;
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                                                                          1793 BP.
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Pred. No. 5.
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Pred.
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                                                                                                                                                                                                                                                                                                     identifying
                                 38.2;
No. 12;
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No. 5.
                                                                                                     38.2;
No. 8.
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No. 8;
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No. 7.
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No. 5;
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3.3;
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.2;
                                          ВB
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                                         2
                                                                                                             12;
                                                                                                                                                                                                                                                                                                     genetic
                                          Length
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                                                                                                             Length
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                                                                                                                                                                                                                                                                                                       disorders)
                                                                                                                                                                                                                                                                                                                                                                                                                            388;
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A2.

JUNE 1 GENENTECH

JUNE 2 MATCH

Best Local Similarity

RESULT 573

ID ADK14120 stand

PN US200

PD US200
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Guery Match
Best Local Similarity
RESULT 566
ID ADSESSOR
                                                                                                                         Best Local Similarity RESULT 572
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Best Local Similarity
RESULT 571
                                                                                                                                                                                                                                                                                                                                                                   Best Loc
RESULT 569
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RESULT 568
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Best Local Similarity
RESULT 567
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                                                                                                                                                                                                                                                                                                                                                                Prokaryotic essential gene #6732.
W0200277183-A2.
03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
uery Match 2.6%; Score
est Local Similarity 47.0%; Pred. 1
TLT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACA23764 standard; DNA; 2421 BP. prokaryotic essential gene #5421. WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial polynucleotide US2003233675-A1.
             ADK14120 standard; cDNA; 4139 BP.
Human autoimmune disorder gene #2
US2003228617-A1.
                                                                                                                                                                                                                                                       Human src biomar W02003062395-A2.
                                                                                                                                                                                                                                                                                                                                    Hypoxia-induced WO200246465-A2.
                                                                                          ADP24081 standard; cDNA; PRO polypeptide encoding WC2004041170-A2.
                                                                                                                                                                          Antipsoriatic cDNA
WO2004028479-A2.
                                                                                                                                                                                            ADN04316 standard;
                                                                                                                                                                                                                                                                           ADD14797 standard;
                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK
ry Match
t Local Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                         ABV77934 standard;
                                                                                                                                                               08-APR-2004
                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBE 2.6%; Local Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                            13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHEN X.
GOLDMAN B
                                                                                                                                                                                                                                                                 biomarker
                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                   cDNA; 3250 BP.
sequence #358.
                                                                                                                                                                                                                                                                                                                                                         DNA;
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                                                                                                                                                                                                                                                               cDNA; 3250 BP.
polynucleotide
                                                                                                                                   2.6%;
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                                                    492
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#7092.
                                                                                                     3250
CDNA
                       gene #24
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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No. 17;
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No. 14
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No. 14;
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No. 17
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No. 17;
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No. 14
                                                                                                       NO:1259
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                                                                13;
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BESULT 576
                                                                                                          Best Local Similarity
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Best Local Similarity
RESULT 574
  닮당
                      RESULT 582
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                                            Query Match
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                                                                                                                                                                                                                                                                        AAA31969 standard; DNA; 345 Plant microsatellite marker WO9967421-A1.
                                                                                                                                                                                                                                                                                                                                                             ACN44936 standard; DNA; 50460 BP. Mouse genomic sequence mCG5738. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP25280 standard; cDNA; 5019 PRO polypeptide encoding cDNA WO2004041170-A2
AAA31454 standard; DNA; 404 Plant microsatellite marker
                                                                         DNA encoding novel WO200175067-A2.
                                                                                                AAS74660 standard;
                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FOREST LTD. 2.6%; Score 38; Score 38; Local Similarity 49.0%; Pred. No.
                                                                                                                                                                         Plant microsatellite WO9967421-A1.
                                                                                                                                                                                               AAA31680 standard;
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(PLET-) FLETCHER CHALLENGE FOREST EXP MAtch 2.6%; Score Local Similarity 49.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human zygote arrest
WO2003091400-A2.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ63176 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
ry Match 2.6%; Score 38.2;
t Local Similarity 49.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 4574.
WO200142467-A2.
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                                                                                                                                                                                                                                                               29-DEC-1999
                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY.
ry Match 2.6%;
Local Similarity 54.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                     HYSE-) HYSEQ INC.
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                                ocal Similarity
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te marker
                                                                                   cDNA; 381 BP.
human diagnostic
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49.8%;
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53.9%;
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(Zar1)
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nucleotide sequence
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#641.
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#930.
                                                                                                                    Score 38;
Pred. No.
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Pred.
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SEQ ID NO:2458
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No. 65;
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No. 21;
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No. 19;
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No. 25;
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                                         Length 381;
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Query Match
Best Local S
RESULT 590
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Best Local Similarity
RESULT 583
          Best Loc
RESULT 591
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RESULT 584
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Zea mays DNA fragment SEQ ID NO: 30519
EP1033405-A2.
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V8-FBB-2002.

(SCRI ) SCRIPPS RES INST.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

48.6%; Pred.
                                                        ADC77186 standard; DNA; 617 DNA homologous to phytopatho W02003020905-A2.
                                                                                                                                                                                                                                 WO2003020905-A2.
                                                                                                                                                                                                                                                                                           06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana stress
WO200216655-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9967421-A1.
                                                                                                                     (DOWC ) DOW
                                                                                                                                                   WO2003020936-A1.
                                                                                                                                                           ADK55194 standard; DNA; 560 BP.
Plant DNA sequence which confers altered metabolic characteristic #2577.
                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                          EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                   AAC49319 standard; DNA; 456 BP.
Arabidopsis thaliana DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
ry Match 2.6%; Score 38;
t Local Similarity 48.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana gene,
WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA68519 standard; DNA; 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ14848 standard; DNA; 450
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ADK56996 standard; DNA; 617
                                       (DOWC
                                                                                                                                       13-MAR-2003
                                                                                                                                                                                                             (DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                    ADC76485 standard;
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                                                                                          ABL68262 standard; DNI
Kidney cancer related
WO200194629-A2.
                                                                                                                                                          ADJ57067 standard; DNA; 13535 BP. Vector plasmid pEE 15.1 hCMV/GFP+hot W02004009823-A1.
                         Lung cancer related gene sequence WO200194629-A2.
                                         ABL66947 standard; DNA; 62944 BP
                                                                                                                                                                                                                                     Gene encoding a subunit JP2000060568-A.
                                                                                                                                                                                                                                                                                                      Human immune system WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana polynucleotide SEQ ID NO US2002059663-A1.
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2.6%;
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MATHEW A V.

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US2003073623-A1.
17-APR-2003
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                                                                                                                     ACH28432 standard; cDNA; 455
Human adult ovary cDNA #6812
US2003073623-A1.
ACH17443 standard; cDNA; 459 BP.
Human adult heart cDNA #1757.
US2003073623-A1.
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US2003073623-A1.
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Human adult heart cDNA #2551.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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JONES L W.
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Tumour-associated;
WO2004030615-A2.
ADJ56207 standard; cDNA; 1 Human cDNA differentially US2003119009-A1.
                                                                   AAI93806 standard; cDNA; 1306 BP.
Human polynucleotide SEQ ID NO 13866.
WO200164835-A2.
                                                                                                                                         WO200166689-A2.
                                                                                                                                                 cDNA encoding novel
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Human differential transcription-associated
W0200157058-A2.
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(LABA/) LABAT I.
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(DICK/) DICKSON M C.
(JONE/) JONES L W.
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Human adult heart cDNA #386.
US2003073623-A1.
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Query Match
Best Local S
RESULT 614
ID ACA26293
DE Prokaryot
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RESULT
            Best Loc
RESULT 622
                                                                                               Best Local Similarity RESULT 621
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Best Local Similarity
RESULT 617
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RESULT 615
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2003.
(STUA/) STUA
(NUCH/) NUCH
(PLON/) PLON
                                                                                                                                                   Human kinesin-like
US6455293-B1.
                                                                                                                                                                                              (CYTO-) CYTOKINETICS INC.
Pry Match 2.5%;
It Local Similarity 44.0%;
                                                                                                                                                                                                                                                   DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice gene, SEQ I
WO2003000898-A1.
                                                                Human SCAP encod WO2003008625-A2.
                                                                        ACC47237 standard; cDNA; 5197 BP.
Human SCAP encoding cDNA-Incyte Id.
                                                                                                                                                            ABS57218 standard; DNA; 4911
Human kinesin-like protein, 1
                                                                                                                                                                                                                              US6383796-B1.
07-MAY-2002.
                                                                                                                                                                                                                                                                                                         30-JUL-2002.
(CYTO-) CYTOKINETICS INC.
                                                                                                                                                                                                                                                                                                                                         ABQ81185 standard; cDNA; 491
Human kinesin motor protein
                                                                                                                                                                                                                                                                                                                                                                         (CNRS ) CENT NAT RECH SCI.
ry Match 2.5%;
t:Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     EP600136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ65476 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
xy Match 2.5%;
t Local Similarity 49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breast cancer re
US2003099974-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS AG

XY Match 2.5%; Score

L Local Similarity 50.3%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
xy Match 2.5%;
t Local Similarity 52.2%;
  ABX11086
                                            (INCY-)
                                                                                                                                                                                                                                                               ABK52651 standard;
                                                                                                                                                                                                                                                                                                                               US6426193-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACN90405 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA71195 standard; DNA; 1839
Rice gene, SEQ ID 4518.
                                                                                                                               (CYTO-) CYTOKINETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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NUCHTERN J G
PLON S E.
SHOHET J M.
                                           INCYTE
                     Similarity
standard, DNA; 42999
                                                                                                                                                                                                                                                                                                                                                                                                                           andard; DNA; 3
adrenergic i
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                    E GENOMICS INC.
2.5%;
arity 44.0%;
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related marker,
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                                                                                                         2.5%;
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49.3%;
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HsKif21b
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Pred.
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No. 23;
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No. 16;
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No. 26;
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No. 26;
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No. 14
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No. 26;
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No.
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No. 14
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22;
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(rrna)

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Best
RESULT
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Best Local Similarity
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                                      WO2003020936-A1.
                                                Plant DNA sequence
                                                                                                                        ADK57005 standard;
Plant DNA sequence
WO2003020936-A1.
                                                                                                                                                                                                 ADC75911 standard; DNA; 526 BP. DNA homologous to phytopathogen WO2003020905-A2.
                                                                                                                                                                                                                                                                  ADC77195 standard; DNA; 526 BP. DNA homologous to phytopathogen WO2003020905-AZ.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                      Murine carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC85413 standard;
Mouse Braf genomic
WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB72671 standard;
Mouse Braf gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA02933 standard; DN Mouse Braf carcinoma WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ribosomal RNA US2002160410-A1.
                                                        ADK55189 standard;
                                                                                            (DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                                              L3-MAR-2003.
(DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                               US2004072154-A1.
                                                                                                                                                                                                                                                         (DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                 MORR/) MORRIS D W. (ENGE/) ENGELHARD E
                                                                                                                                                                                                                                                                                                                                                                                1DM74528 standard; DNA; 96599
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TY Match 2.5%;
Local Similarity 54.7%;
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2.5%;
Similarity 54.7%;
           DOW CHEM
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th 2.5%;
Similarity 54.7%;
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CHEM CO.
I AGROSCIENCES I
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                                               DNA; s
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3 LLC.
                                               526 BP.
h confers
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37.6;
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No. 9.
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No. 9.
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No. 9.
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No. 1.
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No. 1
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No. 78;
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1.9;
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.2e+02;
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.2e+02;
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.2e+02;
                                               metabolic
                                                                                                                                  metabolic
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.2e+02;
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                                                                                                                                  characteristic #4388.
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                                               characteristic
                                                                                                                                                                                                                                                                                     CDNA
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B E I
                             Best Local Similarity RESULT 639
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RESULT 637
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RESULT 636
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RESULT 635
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RESULT 634
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RESULT 633
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RESULT 632
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                                                                                                                                                                  Pseudomonas ae
US6551795-B1.
22-APR-2003.
                                                                                   ADD00948 standard; cDNA;
Human Jagged 2 encoding w02003077848-A2.
                                                                                                                                                                                                                                                                  ABD06577 standard; DNA; 1794 BP.
Pseudomonas aeruginosa polynucleotide #5181.
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                   ABD06635 standard; DNA; 1344 BP.
Pseudomonas aeruginosa polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNI-) UNIV JAPAN OKAYAMA.

"YY Match 2.5%;

It Local Similarity 49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA clone origin. WO2003057877-A1.
                  ADH62908 standard;
                                                                                                                                                        (GENO-)
                                                                                                                                                                                                  ABD06690 standard;
                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS

ry Match
2.5%;
t Local Similarity 51.2%;
                                                                                                                                                                                                                                                        22-APR-2003
                                                                                                                                                                                                                                                                                                                                                            US6551795-B1.
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US2003233675-A1.
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DNA clone originating in barley containing SNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNI-) UNIV JAPAN OKAYAMA.
xy Match 2.5%;
t Local Similarity 49.0%;
                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
ry Match 2.5%; Scor
t Local Similarity 51.2%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS51517 standard;
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ry Match 2.5%;
t Local Similarity 49.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
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SLATER S
                                                               ISIS PHARM
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polynucleotide
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aeruginosa polynucleotide
         DNA
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                                                 TINC.
       DNA;
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                                         2.5%;
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cDNA S
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n barley
                     4749
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#6260.
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barley
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                                                                                                                                 S CORP.
; Score 37.6; I
; Pred. No. 22;
                                         Score
Pred.
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SEQ ID
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Pred.
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Pred.
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Pred. No. 16;
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                                         No. 30;
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No. 11;
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No. 11;
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SABB
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Best Local Similarity
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Human jagged 2, JAC
WO2004076682-A2.
                                                                                                                                                                                                                                                                                                                                                                                         ADH57070 standard; DNA; DNA of a human Jagged 2 US2003207839-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD00955 standard; cDNA; 4974 Human Jagged 2 encoding cDNA; WO2003077848-A2.
WO2004074320-A2.
                 Mouse cancer-associated genomic DNA MD12-017
                                                                                    WO2004074320-A2.
                                                                                             ABD32870 standard; DNA;
Mouse cancer-associated
                                                                                                                                                                                                    (NAAD-) NAT INST ADVANCED IND 2.5%; St Local Similarity 52.6%; F
                                                                                                                                                                                                                                          ADR83400 standard;
Human jagged 2 DNA,
WO2004076622-A2.
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Antipsoriatic cDNA sequence #1
WO2004028479-A2.
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Human Jagged 2 DNA
US2003170636-A1.
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DNA of a human Jagged 2
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                           ABD32610 standard; DNA; 115780 BP
                                                                                                                                            (SURR-) SURROMED
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52.6%;
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RNA seque
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genomic DNA MD17-083
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Best Local Similarity
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RESULT 654
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RESULT 651
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RESULT 656
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RESULT 650
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Best Local Similarity
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(OENE-) GENE LOGIC INC.
2.5%;
Match 'arity 47.0%;
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
2.5%;
ery Match 2.5%;
46.0%;
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                                                                                                                                                                                                                                                      ADB68842 standard; DNA; 536 BP. Minority lux1 consensus sequence WC2003057902-A2.
                                                                                                                                                                                                                                                                                                                                                      ADB53812 standard; DNA; 511 BP.
Primary rat hepatocyte toxicity modelling
W02103065993-A2.
ACL19199 standard; DNA; DNA clone originating in WO2003057877-A1.
                                         (UYNI-) UNIV JAPAN OKAYAMA.

ry Match 2.5%;
t Local Similarity 49.2%;
                                                                                               ACL19219 standard; DNA; 593 BP. DNA clone originating in barley
                                                                                                                               (UYNI-) UNIV JAPAN OKAYAMA.

ry Match
t Local Similarity 49.2%;
                                                                                                                                                                           DNA clone originating WO2003057877-A1.
                                                                                                                                                                                                  ACL19217 standard; DNA;
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Human genomic sequence l
WO2003073826-A2.
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(APPA/) APPARSUNDARAM S.
(FERG/) FERGUSON S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY INC.
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th 2.5%;
Similarity 13.4%;
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47.0%;
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No. 11;
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No. 11;
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No. 1.
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No. 2.1e+02;
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           #9190.
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Query Match
Best Local S
RESULT 666
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RESULT 664
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Best Local S
RESULT 659
ID ACL19201
DE DNA clone
PN W02003057
PD 17-JUL-20
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Best Local Similarity
RESULT 661
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                                                                              DNA clone originating in WO2003057877-A1.
ACL19216 standard; DNA; 670 BP. DNA clone originating in barley containing WO200305787-A1.
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                                                                                                                                                               DNA clone originating WO2003057877-A1.
                                                                                                                                                                                   ACL19221 standard;
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17-JUL-2003.
(UYNI-) UNIV JAPAN OKAYAMA.
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ARY Match 2.5%;
49.2%;
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(UYNI-) UNIV JAPAN OKAYAMA.
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                                                                  (UYNI-) UNIV JAPAN
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ry Match 2.5%;
t Local Similarity 49.2%;
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ry Match
t Local Similarity 49.2%;
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2.5%;
49.2%;
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n barley containing
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                  SNP encoding sequence
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Best Local Similarity
RESULT 667
ID ACTION
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RESULT 671
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RESULT
ID AC
                          Best Local Similarity RESULT 674
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RESULT 669
                                                                                                                                                                                       Query Match
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                                                                            ADQ63696 standard; cDNA; 2336 BP. Novel human cDNA sequence #857.
                                                                                                                                           Human HIPHUM GB2365432-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP29084 standard; DNA; 1044 BP. Human secreted protein encoding WO2004035732-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA clone originating in barley WO2003057877-A1.
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                                                                    EP1440981-A2.
                                                                                                                                                                                                                 ABX72264 standard; cDNA; iHuman NOVX polynucleotide WOZ00281498-A2.
Human neurotransmitter transporter
WO2003059947-A1.
                 ACF79238 standard;
                                                                                                                                                             AAD34007 standard;
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                                                    (REAS-) RES
                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                        17-OCT-2002
                                                                                                                                                                                                                                                                                        (PROV,
                                                                                                                                                                                                                                                                                                (KATA/
                                                                                                                                                                                                                                                                                                                                  (BRIG/)
                                                                                                                                                                                                                                                                                                                                                                              US2004016025-A1.
                                                                                                                                                                                                                                                                                                                                                                                               ADJ39564 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-2004
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ry Match 2.5%;
t Local Similarity 49.2%;
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xy; Match
t Local Similarity 49.2%;
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                                                         GLAXO
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KATAGIRI F.
KREPS J.
PROVART N.
                                ASSOC BIOTECHNOLOGY.
2.5%; Scoilarity 53.8%; Pre
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                                                                                                                         GROUP LTD.
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2.5%; Sco
47.6%; Pre
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2.5%;
49.2%;
                 CDNA; 2388 BP
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re 37.4;
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                                                                                                                                                                               No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 13;
                                   No.
                                          37
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No
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        variant
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No. 13
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23;
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21;
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        polymucleotide.
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                                           2336;
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Best Local Similarity
RESULT 682
ID ABD17123 standard; D
DE Pseudomonas aerugino
PN US6551795-B1.
PD 22-APR-2003.
                                                                                                                                                            Query Match
Best Local Similarity
RESULT 681

ID ABD17057 standard; D)
DE Pseudomonas aerugino
PN U86551795-B1.
PD 22-APR-2003.
                                RESULT
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  PRE
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Best Local
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                                                                                  ABD17123 standard; DNA; 1428 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                                                                                                                                                     AAC56719 standard;
Eucalyptus grandis
WO200053724-A2.
ABK92063 standard;
DNA encoding novel
WO200229058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ97161 standard; DNA; 107432 BP. Mouse cancer associated sequence MD08-009, WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC43635 standard; DNA; 2490 BP. Nucleotide sequence of the human FR2828209-A1.
                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                               (GENES.) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
ry Match 2.5%; Score 37.2;
t Local Similarity 49.0%; Pred. No. 1:
                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                 AAI84688 standard;
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(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human neurotransmitter WO2003059947-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER AG
                                        (GENO-) GENOME THERAPEUTICS 2.5%; Local Similarity 44.7%;
                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 679
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                                                                                                                                         Match
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th 2.5%; Scor
Similarity 44.7%; Pred
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                                                                                                                                                                                                                                                                                                                                                                      CDNA; 439 BP.
de SEQ ID NO 4748.
          DNA; 1782 BP. transmembrane
                                                                                                                                                                                                                                                                                transcription
                                                                                                                                                                                                                                                                                           DNA; 476
                                                                                                                                                                                                                                                                                                                 2.5%;
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polynucleotide
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          segment 2-like
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                                         37.2; I
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No. 12;
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No. 24;
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No. 1.
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No. 24;
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No. 24;
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                                                                                              #15727
                                                                                                                                                                                 #15661
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                                                                                                                                                                                                                                                                                 #590
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Query Match
Best Local Similarity
RESULT 687
                                       RESULT 686
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ABD17019
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Human NOVX protein Nov45D ger
US2004014053-A1.
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18-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOV45d gene
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                          (SHEN
                                                                                                                                                                (SPYT,
                                                                                                                                                                                    (LEIT
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(PATT/)
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) GUO X S.
) ANDERSON D W.
SPYTEK K A.
GERLACH V.
BURGESS C E.
KHRAMTSOV N V.
                        TAUPIER R
CATTERTON
SHENOY S G
                                                                                        RASTELLI L.
AGEE M L.
CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
                                                                                                                                                                                                                  ZHONG M.
CASMAN S J.
VOSS E Z.
BOLDOG F L.
PADIGARU M.
SMITHSON G.
                                                                                                                                                                                                                                                                     MILLER C E.
RIEGER D K.
PENA C E A.
SHIMKETS R !
                                                                                                                                                                                                GORMAN L.
VERNET C !
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                                                          SPADERNA S
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                                              TIU X
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standard; DNA; 2679
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                       G. H.
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Pred. No. 2
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No. 2
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No. 23
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                   Length
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                   1881;
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Query Match
Best Local S
RESULT 691
                               Best Local Similarity RESULT 696
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RESULT 694
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Best Local Similarity
RESULT 690
                                                                                                                  Best Local Similarity RESULT 695
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Best Local Similarity
RESULT 688
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(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
EPID-) SPIDAUROS BIOTECHNOLOGIE AG.
2.5%; Score 3
2-5%; Score 3
2.5%; Pred. 1
                                  12-SEP-2003.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
2:Ty Match 2.5%;
51Y Match 53.4%;
                                                                                                                                                                                                                 Human CYP1A2 gene SEQ ID NO:76. WO2003014387-A2.
                                                                                                                                                                                                                                                                                                   Murine cancer-associated (CA) W02004058146-A2.
Maize sucrose s
US2003135870-A1
                     ADA58478 standard;
                                                                                ACN45182 standard; DNA; 261817 E Human genomic sequence hCG14925. WO2003073826-A2.
                                                                                                                          Human secreted protein gene sequence, SEQ ID No ry Match 2.5%; Score 37.2; DB 8; L Local Similarity 48.6%; Pred. No. 1.6e+02;
                                                                                                                                                           AAL51405 standard; DNA; 80959 BP.
                                                                                                                                                                                                                                                                                                                                                                                     ADJ31073 standard; DNA;
Human musculoskeletal sy
US2004009488-A1.
15-JAN-2004.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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RESULT 699
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RESULT 703
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RESULT 700
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(CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                              Pseudomonas aeruginosa polynucleotide US6551795-B1. 22-APR-2003.
                                                                                                                                                                                                                                       ACA23920 standard; DNA; 1092 Prokaryotic essential gene #5 W0200277183-A2.
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22-APR-2003.
(GENO-) GENOME THERAPEUTICS
ery Match
2.5%;
ery Match
45.6%;
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22-APR-2003.
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(ELIT-) ELITRA PHARM INC.
2.5%;
ry Match
2.5%;
t Local Similarity 53.9%;
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Zea mays DNA fragment SI
EP1033405-A2.
  Nucleotide sequence
                               (GENO-) GENOME THERAPEUTICS ry Match 2.5%; t Local Similarity 45.6%;
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WO2004072281-A1.
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             AAF85145
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WO200266501-A2.
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xy. Match 2.5%;
t Local Similarity 48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACL19215 standard; DNA; 439 BP. DNA clone originating in barley WO2003057877-A1.
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US6551795-B1.
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standard; DNA; 1800 BP.
de sequence of the relaxase virD2.
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polynucleotide
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Best Local Similarity

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03-MAY-2001.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
2.5%; Score 37; DB 4; Lo
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(INMR) MERIEUX ORAVAX PASTEUR MERIEUX (HUMA-) HUMAN GENOME SCI INC.
                            Human kinase genomic US2003175927-A1.
                                     ADJ37690 standard; DNA; 90541 Human kinase genomic DNA.
                                                                                                                                          ABS52847 standard; DNA; 90541 BP. Human SR protein-specific kinase 2, US2002094560-A1.
                                                                                                                                                                                                                       WO2003097685-A1.
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Human USH3A gene genomic sequence
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WO9843478-A1.
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                (ABUT/) ABU-THREIDEH (GONG/) GONG F.
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th 2.5%;
Similarity 57.3%;
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1.3e+02;
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27;
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1.9e+02;
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1.4e+02;
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Length 90541;
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Best Lo
RESULT 71
 Query Match
Best Local Similarity
RESULT 716
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                                                                                                                                                                                      Human genome derived s
US2003194704-A1.
16-OCT-2003.
(PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize sucrose synthase EST #326. US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                  AAC36202 standard; DNA; 5 Arabidopsis thaliana DNA EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR31219 standard;
Human SRPK2 kinase
                                                                                                                                                                                                                                                                                                                    ACH78156 standard; DNA; 518 Human genome derived single US2003194704-A1.
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(GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA sequence WO200151659-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH88704 standard;
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                                    (MATH/
                                                                                                                                   US2002059663-A1.
                                                                                                                                             Arabidopsis thaliana polynucleotide SEQ ID NO
                                                                                                                                                     ABQ66069 standard; DNA; 636
                                                                                                                                                                                                                                              ACH78575 standard; DNA;
                                                                                                                                                                                                                                                                               (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APPL-) APPLERA CORP.
                                                                                                            (/YYWA)
                                                                                                                                                                                                                                                               Local Similarity
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
                                                                              PRICE J L.
RAINES T M.
                                                    RAMEAKA J G.
PAGE A.
                                                                                                 HAMILTON C M.
                                                                                                                  GORLACH J.
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protein
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SEQ ID
                                                                                                                                                                                                                                    NA; 518
single
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52.2%;
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No.
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1.9e+02;
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2.5e+02;
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Best Local Similarity RESULT 726
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Best Local Similarity
RESULT 722
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ABL68609 standard;
Kidney cancer relat
WO200194629-A2.
                                                                                                                                                                                                             Stealth virus nucleic acid clone, 2.5%; Score 2.5%; Score 2.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                  AAT62440 standard;
Human L5/3 growth 1
US5606029-A.
                                                                                                                                                                             AAQ79728 standard; DNA; 6100
Human L5/3 tumour suppressor
                                                                                                                                                                                                                                                                                                         ABL06732 standard; cDNA; 4298 BP. Drosophila melanogaster expressed W0200171042-A2.
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Pseudomonas aeruginosa polynucleotide #2045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF82218 standard; DNA;
Melon ethylene receptor
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                                                                                                                          (CHIL-) CHILDRENS HOSPITAL MEDICAL ry Match 2.5%; Score Local Similarity 55.5%; Pred.
                                                                                                                                                                                                                                            AAX84332 standard; DNA; 5059 BP.
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(PEKE ) PE CORP NY.
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                                                             (CHIL-) CHILDREN'S
                                                                                                                                                                                                                                                                                                                                                                                                                   ABD03441 standard;
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                                        ocal Similarity
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) DAVIS K R.
) ALLEN K.
) HOFFMAN N.
) HURBAN P.
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h
Similarity 49.5%;
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        lard; DNA; 9980 BP.
related gene sequence
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                                                              HOSPITAL
                                        2.5%;
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gene
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                                      MEDICAL CENT.
Score 36.8; DB
Pred. No. 56;
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promoter-related
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re 36.8; DB
d. No. 51;
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36.8;
No. 56;
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No. 38;
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No. 33;
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No. 47;
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No. 18
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           NO:6946.
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RESULT 732
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RESULT 735
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RESULT 733
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Best Local Similarity
RESULT 730
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(GENE-) GENE LOGIC INC. 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (STATE TO THE TOTAL 2.5%; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypermethylation site in human US2003129602-A1.
                                        ACA64924 standard; DNA; 201239 Human PLZF DNA corresponding to DE10127572-A1.
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                                                                                                                                                                                                                        WO200228999-A2.
                                                                                                                                                                                                                                         ABK83562 standard; cDNA; 1
Human cDNA differentially
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2.5%;
It Local Similarity 69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                             ADI37256 standard; DNA; 118067
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Murine TGF-beta binding protein (BEER)
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                                                                                                                                                                               (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUAN/) HUANG T H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP45591 standard; DNA; 92500 BP.
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US6582946-B1.
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                       PATHOARRAY
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GMBH.
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56.7%;
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55.5%;
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Y expressed
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liver cancer.
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Score 36.8; DB 12; Length 9;
Pred. No. 2.2e+02;
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Score
Pred.
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Pred. No. 1.8e+02;
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Pred.
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Pred.
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BC) locus-37.
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breast
                                                                                AF060568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic
                                                                                                                                                                                                                                                                                                        36.8;
No. 2.
36.8;
                                                                                                                                         36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.8; 1
No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.
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No. 1.
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2
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1.
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                                                                                                                                                                                                                                                                                                        DB 12;
.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
.4e+02;
                                                                                                                                         DB 6;
.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
.8e+02;
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.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
.4e+02;
  DB
                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA.
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                                                                                                                                                              Length 139904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         island
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                                                                                                                                                                                                                                             cells
  201239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92500;
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Score

Length

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RESULT 746
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RESULT 743
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                                                                                                                                                                                                                                                                                                                                                    ADA48906 standard; DNA; 689 BP. Wheat gene conferring disease resistance in W02003000906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize sucrose synthase US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize sucrose sy US2003135870-A1.
                           WO200146387-A1.
                                    AAH74539 standard; o
Nucleotide sequence
                                                                                                                                                                                                          ADJ41713 standard; cDNA; 689
Plant cDNA #2713.
                                                                                                                                                                                                                                                                                   Wheat DNA sequence
                                                                                                                                                                                                                                                                                              ADC08648 standard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002137160-A1.
26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX52791 standard; cDNA; 438 BP.
Bovine EST associated with lactation/muscle/fat deposition #2720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA58461 standard;
                                                                                                                                                                                                 JS2004016025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.

CY Match 2.5%; Score

Local Similarity 49.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                           TAON/) TAO N. WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DA58383 standard; cDNA;
                                                                                                                                                                                                                                                        SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                              BYAT/) BYATT J C.
MATH/) MATHIALAGAN
                                                               ocal Similarity
                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
                                                                                                                                       BUDWORTH P.

MOUGHAMER T.

BRIGGS S P.

COOPER B.

GLAZEBROOK J.
                                                                                  RICKE D.
ZHU T.
                                                                                                   PROVART N.
                                                                                                                      GOFF S A.
KATAGIRI F.
        CORNELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase
         RES
                                                                                                                                                                                                                                                                                   DNA; 689 BP.
Seg ID953 related to grain
                                    cDNA; 905 BP.
e of a chitobiosidase
2.5%; Score
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49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IA; 340 BP.
EST #27.
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                                                                Score
Pred.
                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                      Score 36.6;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                          Score 36.6;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.6;
Pred. No. 15;
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No. 22;
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No. 22;
36.6;
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No. 14
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                                    polypeptide
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                                                                         12;
Length 905;
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 438;
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                                                                         Length
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Query Match
Best Local S
RESULT 748
                                                         Best Loca
RESULT 754
                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                   Best Local Similarity RESULT 752
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SULT 747
                                                                                                                                                                            Query Match
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                                                              01-JUL-2004.
01-JUL-2004.
(KYOW ) KYOWA HAKKO KOGYO KK.
2.5%;
ery Match
2.5%;
                                                                                                                 ADQ25850 standard; DNA; 4145 BP. Rat G-protein coupled receptor 88 W02004054617-A1.
                                                                                                                                                                                                               Nucleotide sequence WO200146387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA47947 standard; DN Rice gene conferring WO2003000906-A2.
                                                                                                                                                                                                                                                                                                           AAZ06824 standard; DNA; 1294 BP.
Streptomyces albidoflavus chitobiosidase DNA
W09942594-A1.
           AAH41184 standard; DNA; 4164 BP. Rat G protein-coupled receptor, WO200136634-A1.
25-MAY-2001.
                                                                                                                                                                                                                          AAH74537 standard; DNA; 1294 BP.
Nucleotide sequence of a chitobiosidase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice DNA sequence WO2003000905-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice gene, SEQ I
WO2003000898-A1.
                                                                                                                                                                                                     28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC07965 standard;
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Rice gene, SEQ ID 2714.
                                                                                                                                                                                                                                                                                      (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004016025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ39882 standard; cDNA; 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOUG/
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                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                    RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                          GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNGENTA PARTICIPATIONS
th 2.5%; Sco.
Similarity 49.7%; Pre
                                                                                                                                                               CORNELL RES FOUND INC.
h 2.5%; S
Similarity 50.9%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNGENTA PARTICIPATIONS AG. h 2.5%; Score 36.6; Similarity 49.7%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLAZEBROOK J.
CENT ADVANCED SCI & TECHNOLOGY INCUBATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DNA; 1182 BP.
Seq ID231 related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ng disease
                                                                                                                                                                                                                                                             2.5%;
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49.7%;
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                                                                                                                                                                 Score
Pred.
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resistance
                                                                                                                                                                                                                                                              Score 36.6;
Pred. No. 29;
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Score
Pred.
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Pred.
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                                                                    Score 36.6;
Pred. No. 53;
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Pred.
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                                 Strg, coding sequence
                                                                                                                            coding sequence
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No. 28;
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No. 28;
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No.
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29;
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28;
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                                                                              Length 4145;
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Best Loca
RESULT 758
SEE
                                      RESULT 763
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RESULT 759
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RESULT 755
                                                                                                                     RESULT 762
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                                                                                                                                                                                                                        Query Match
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        ADA69502 standard; DNA; 450 Rice gene, SEQ ID 2825. WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE59567 standard; DNA; Human gene XM 038377, SI WO2003016475-A2.
                                                                                      DNA clone originating WO2003057877-A1.
                                                                                               ACL19207 standard; DNA; 418 BP. DNA clone originating in barley
                                                                                                                                                                             ACL19211 standard; DNA; 409 BP.
DNA clone originating in barley containing
                                                                                                                                                                                                                                                   Maize gene confe
WO2003000906-A2.
                                                                                                                                                                                                                                                                                                                                 Human secreted protein encoding sequence W02004035732-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 Corn seedling-derived polynucleotide US2003237110-A9.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS70697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN44528 standard; DNA; 49806 BP Mouse genomic sequence mCG20647. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE59563 standard; DNA;
Human gene XM_038377, SI
WO2003016475-A2.
                                                                                                                                                                       WO2003057877-A1.
                                                                                                                                                                                                                                                                        ADA49220 standard;
                                                                                                                                                                                                                                                                                                                                                      ADP29106 standard; DNA;
                                                                                                                                               (UYNI-) UNIV JAPAN OKAYAMA.
                                                                                                                                                                                                           (SYGN) SYNGENTA PARTICIPATIONS AG.

TY Match 2.5%; Score

Local Similarity 52.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO ) GEN HOSPI
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPI
(FARB ) BAYER AG.
                                                                   UYNI-) UNIV JAPAN
                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                             FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                              Local Similarity
                                               Local Similarity
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th 2.5%;
Similarity 57.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEN HOSPITAL
                                                                                                                                                                                                                                                             conferring
                                                                   OKAYAMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 272
                                               2.5%;
                                                                                                                              2.5%;
                                                                                                                                                                                                                                                                                         2.5%;
                                                                                                                                                                                                                                                                                                                                                                        1 INC.
2.5%;
58.1%;
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disease re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 5761
SEQ ID
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SEQ ID
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Pred. No. 53;
                                                                                                                                                                                                                                                              resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5459.
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                                                                                                containing
                                                                                                                                                                                                                                                                                       36.4;
No. 16
                                               36.4;
No. 19;
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No. 1.
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No. 62;
                                                                                                                               36.4;
No. 19;
                                                                                                                                                                                                            36.4;
No. 19;
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62;
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.8e+02;
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                                                         418;
                                                                                                                                        409;
                                                                                                sequence
                                                                                                                                                                               sequence
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Query Match
Best Local Similarity
RESULT 764
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OF THE COLUMN AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AND AGGEOREM AGGEOREM AGGEOREM AND AGGEOREM AGGEOREM AGGEOREM AGGEO
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RESULT 769
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RESULT 768
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SULT 765
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                                                                Banana gene conferring d WO2003000906-A2.
                                                                                                                                                                                                                                              ACL19210 standard; DNA; 517 BP. DNA clone originating in barley W02003057877-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           ADA69813 standard; DNA;
Rice gene, SEQ ID 3136.
WO2003000898-A1.
                                                                                                                                                                                                        17-JUL-2003.
(UYNI-) UNIV JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH22587 standard;
Human adult ovary ous US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE 2.5%; S Local Similarity 55.6%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expression marker WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV59448 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice gene confer
WO2003000906-A2.
                                                                                                                                                                                                                                                                                                                                                                       (SYGN ) SYNGENTA PARTICIPATIONS
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        Local Similarity
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LABAT I.
STACHE-CRAIN
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNGENTA PARTICIPATIONS AG.

th 2.5%; Score
Similarity 48.1%; Pred.
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      PARTICIPATIONS AG.
2.5%; Score
ty 48.1%; Pred.
                                                                                                                                                                 0KAYAMA.
2.5%;
46.7%;
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48.1%;
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                                                                                                        ; 600 BP.
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resistance
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Score
Pred.
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Pred.
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Pred.
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                                                                                                                                                                   Score 36.4;
Pred. No. 21;
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Pred. No. 21;
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                                                                                                          resistance
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No. 2
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No. 20;
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7.4;
23;
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                                                                                                        plants
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CDNA;

909

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Query Match
Best Local S
RESULT 777
                                                                                                                                                                                  PAGRE
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                                                                                      RESULT 776
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Best I
                                                                                             Best Local Similarity
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Plant cDN
ADC77183 standard; DNA; 784 BP. DNA homologous to phytopathogen WO2003020905-A2.
                                                                                                                                                                                                                                                                                                                                                                                                           DNA homologous to WO2003020905-A2.
                                                                   ADC76482 standard; DNA; 784 BP.
DNA homologous to phytopathogen resistance-related
                                                                                                                            DNA homologous to WO2003020905-A2.
                                                                                                                                           ADC75915 standard;
                                                                                                                                                                                                                                                                                                                                                    Plant DNA sequence which confers altered metabolic characteristic #6471.
                                                              WO2003020905-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                          ADC76477 standard;
                                                                                                                                                                                                                                                                        Plant cDNA #3638.
US2004016025-A1.
                                                                                                                                                                                                                                                                                                                                                           ADK59088 standard;
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                                                                                                                                                                                                                                                                                       MJ42638 standard;
                                               (DOWC ) DOW CHEM
                                                                                                                                                                                                                                                                                                                     DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                            DOWC ) DOW CHEM CO
                               Local Similarity
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                                                                                                                                                                                                                       BUDWORTH P.

MOUGHAMER T.

BRIGGS S P.

COOPER B.

GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RICKE D.
ZHU T.
                                                                                                                                                                          RICKE D.
ZHU T.
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KATAGIRI F.
KREPS J.
PROVART N.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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PROVART N.
                                                                                                             DOW CHEM CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
NA #3628.
                                                                                                                                                                                                                                                                                                                                                                                                                  to phytopathogen resistance-related
                                               8
                                                                                                                                  ; DNA; 716 BP.
phytopathogen
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                              2.5%;
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                                                                                                                                                                                                                                                                                        662
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No. 26;
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No. 23;
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No. 24;
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Best Loc
RESULT: 783
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RESULT 778
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(DOWC ) DOW
(DOWC ) DOW
                           Lung cancer related WO200194629-A2. 13-DEC-2001.
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13-MAR-2003.
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                                                                                                               Lung cancer related WO200194629-A2.
                                                                                                                                                                                                                                                                 DNA encoding novel WO200175067-A2. 11-OCT-2001.
                                                                                                                          ABL65422 standard; DNA; 1306 BP.
Lung cancer related gene sequence
                                                                                                                                                                                              Oesophagus cancer
WO200194629-A2.
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Plant cDNA #3632.
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                                                         ABL66524 standard; DNA; 1306
                                                                                              (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                 ABL67798 standard;
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
KATAGIRI F.
KAEPS J.
PROVART N.
RICKE D.
RICKE D.
ZHU T.
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Similarity 48.1%;
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No. 27;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              WO2003102159-A2.
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Human NOV45b gene SEQ ID NO:143.
W02003076642-A2.
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(CURA-) CURAGEN CORP.
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WO2004028479-A2.
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      TAUPIER R J.
CATTERTON E.
SHENOY S G.
                                                                   AGEE M L.
CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
GANGOLLI E A.
                                                                                                                                     ANDERSON D W.
SPYTEK K A.
GERLACH V.
BURGESS C E.
KHRAMTSOV N V.
                                 ROTHENBERG I
SPADERNA S I
HJALT T.
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PATTURAJAN
KEKUDA R.
MILLER C E.
MIEGER D K.
PENA C E A.
SHIMKETS R
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CASMAN S J.
VOSS E Z.
BOLDOG F L.
PADIGARU M.
SMITHSON G.
                                                                                                                 ELLERMAN K.
RASTELLI L.
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VERNET C A M.
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No. 34;
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1710;
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RESULT 793
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Best Local Similarity
RESULT 789
ID ABL67803 standard; D
DE Oesophagus cancer re
PN W0200194629-A2.
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04-SEP-2002.
(ECOP-) ECOPIA BIOSCIENCES II
(ECOP-) ACOPIA BIOSCIENCES II
(ECOP-) C+milarity 50.0%;
                                           ACN44608 standard; DNA; 90043 BP Mouse genomic sequence mCG22175. WO2003073826-A2.
                                                                                                           09-AUG-2001.
(HUMA-) HUMAN
                                                                                                                               AAK79963 standard; DNA; 5714
Human immune/haematopoietic
WO200157182-A2.
                                                                                                                                                                                                                     ACN44094 standard; DNA; 35236 BP Human genomic sequence hCG23314. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                             AAS35076 standard; DNA; 32121 BP. DNA #26 encoding human neoplastic W0200155163-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence #337 encoding now w0200155301-A2.
                                                                                                                                                                                                                                                                                                           Human neoplastic US2003082758-A1.
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                                  L2-SEP-2003
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Similarity 55.6%;
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h 2.5%;
Similarity 54.7%;
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No. 2.2e+02;
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No. 1.
36.4; DB 11;
No. 2.8e+02;
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           Length 90043;
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RESULT 805
ID ADB921
DE Human
PN WO2003
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AAD16230 standard; DNA; 107820 sr.
Human ATP-binding cassette transporter ABCC6
ery Match
2.5%; Score 36.4; DB
ery Match
53.5%; Pred. No. 3e+02;
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ADB20869 standard;
MRP1 based cancer:
WO2003013533-A2.
                                                                                ACF62750 standard; DNA; 186591 BP.
Cancer based on CYP3A5 related polynucleotide SEQ
WO2003013534-A2.
                                                                                                                                                                ADB92111 standard;
Human MDR1 related
WO2003013535-A2.
                                                                                                                                                                                                                                                            ADB96920 standard;
Human MDR1 related
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cy Match 2.5%;
Local Similarity 55.6%;
                                                           (EPID-) EPIDAUROS
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DNA sequence SEQ ID
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Best:Local Similarity RESULT 816
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Human UGT1A1 gene s
WO2003013536-A2.
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(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
2.5%; Score 3
2.5%; Pred. N
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Human UGT1A1 gene
WO2003013536-A2.
20-FEB-2003.
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2.5%; Score 36.4;
                               ADB87939 standard;
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                                                                                                      Human UGT1A1 gene sequence
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2.5%; Score 36.4;
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Best Local Similarity RESULT 824
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RESULT 822
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Human DNA encoding WO200136674-A2.
                    AAD07361 standard;
                                                                                    Human myosin light
WO9936531-A1.
                                                                                                          AAX87371 standard;
                                                                                                                                                 WO200268600-A2.
06-SEP-2002.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                  ABS73398 standard;
DNA encoding human
                                                                                                                                                                                                                                   07-SEP-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                            Human polynucleotide WO200164835-A2.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                   ADA58486 standard; cDNA; 294 BP. Maize sucrose synthase EST #130. US2003135870-A1.
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Human MDR1 related
WO2003013535-A2.
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Human MDR1 related
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Human MDR1 related
WO2003013537-A2.
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(ZENE ) ZENECA LTD.
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ch 2.5%; Score 36.4; DB 10;
l Similarity 53.5%; Pred. No. 4.2e+02;
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GPCR HF1948 mutant
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Best Loca
RESULT 833
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Best Local Similarity
RESULT 832
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Best Local Similarity
RESULT 831
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RESULT 828
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RESULT 827
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Best Local Similarity
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(ASTR ) ASTRJ
(ASTR ) ASTRJ
                                                                                                ADL62786 standard; DNA; 1941 BP. Human ovarian cancer DNA marker
                                                                                                                                                                                                                                                                                                          ADP13398 standard; DNA; 1120 BP. Renal cell carcinoma differentially WC2004048933-A2.
US6551795-B1.
22-APR-2003.
                                                                                       WO200170979-A2.
                                                                                                                                                                    Human soft tissue WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  ADM33386 standard; cDNA;
Human PRO71267 encoding c
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antipsoriatic cDNA
WO2004028479-A2.
08-APR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon adenocarcinoma WO200194629-A2.
                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE ry Match 2.4%; Score 36.2 t Local Similarity 46.9%; Pred. No.
                                                                                                                                                                                        ADQ22648 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL62349 standard; DNA; 1120
                              ABD16767 standard;
                                                                                                                                                   (PROT-) PROTEIN DESIGN LABS
                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN03695 standard;
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(TWIN/) TWINE N C.
(BURC/) BURCZYNSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVAL-) AVALON PHARM.
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SLONI D K.
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                 andard; DNA; 1989 BP.
aeruginosa polynucleotide
                                                                                                                                                                             ; DNA; 1303 BP.
sarcoma-upregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA; 1120 BP
sequence #45.
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UK LTD.
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                                                Score 36.2;
Pred. No. 47;
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Pred. No. 35;
                                                                                                  #20998
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No. 35;
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                    #15371
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GENOME THERAPEUTICS CORP

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RESULT 842
ID AAQ551
DE Pseudo
PN WO9401
PD 20-JAN
PA (FUSO
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ID AAD494
DE Human
PN WO2002
PD 31-OCT
PA (INCY-
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ID AAA384
DE Human
PN EP9992
PD 10-MAY
PA (UYPA-
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                                                                                                                                                                                                                                                            Human intracellular signalling protein coding W02002101008-A2.
                                                                                                 ADL13006 standard; cDNA; 5467 BP.
Human steroid-induced C3A liver cell
US6673549-B1.
                                                                                                                                                                                                                                                                                                                                                  AAA38444 standard; DNA; 2893 BP. Human desmin gene 5' flanking re EP999278-A1.
                                                                                                                                                                                Human vesicle-associated WO200286061-A2.
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EP1293569-A2.
                          AAQ55145 standard; DNA;
Pseudomonas aeruginosa p
                                                                                                                                                                                           AAD49464 standard; cDNA; 5230 BP.
Human vesicle-associated protein-8
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          WO9401583-A1.
20-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                               US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABD16799 standard; DNA; 2637 BP.
Pseudomonas aeruginosa polynucle
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                                                                                                                                        (INCY-) INCYTE GENOMICS INC.
CY Match 2.4%;
Local Similarity 50.3%;
                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC.

CY Match 2.4%;

Local Similarity 59.0%;
                                                                                                                                                                                                                                                                                                       (UYPA-) UNIV PARIS VII. 2.4%; cy Match 2.4%; Local Similarity 52.3%;
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ry Match 2.4%;
Local Similarity 48.3%;
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(REAS-) RES ASSOC
                                                                               INCY-) INCYTE
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EQ ID
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No. 47;
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No. 48
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Query Match
Best Local S
RESULT 846
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RESULT 845
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Best Local Similarity
RESULT:843
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Mouse genomic sec
WO2003073826-A2.
12-SEP-2003.
                                                                                                                                              ADL91929 standard; DNA; 15872
Streptomyces venezuelae vep OF
US2003194784-A1.
                                                                                                                                                                                                                                             AAZ87283 standard; DNA; 15872 BP. S. venezuelae vep ORF 1, SEQ ID N WO200000620-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa microbe identification-related WO200299133-A1.
                                                                                                                                                                                                                                                                                                                                                             AAT68715 standard; DNA; 15872 BP.
Streptomyces venezuelae polyketide synthase vep
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Bovine DGAT gene SI
WO2003004630-A2.
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"Y Match 2.4%; Score 36.2; DB 10;

t Local Similarity 50.9%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ77045 standard;
Bovine DGAT gene SI
WO2003004630-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine DGAT1 gene.
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                                     ACN44556 standard;
                                                                                                (SHER/) SHERMAN D H.
(LIUH/) LIU H.
(XUBY/) XUB Y.
                                                                                                                                                                                                                         (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                       06-JAN-2000
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                                                                                       (ZHAO/)
                                                                                                                                                                                                                                                                                               ocal Similarity
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th
2.4%; Score 36.2; DB 10;
Similarity 50.9%; Pred. No. 1.2e+02;
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th 2.4%;
Similarity 44.5%;
                                                                                    ZHAO L.
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gene SEQ ID NO:1.
                       dard; DNA; 22262 BE
sequence mCG21411.
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SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                               2.4%;
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designated PS-2.
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Pred. No. 1.3e+02;
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.le+02;
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SAGRES DISCOVERY

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RESULT 855
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RESULT 854
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Best Local Similarity
RESULT 852
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                                                                                  ABD32868 standard; DNA; Human cancer-associated WO2004074320-A2.
ADQ19085 standard; DNA; 452 Bp.
Human soft tissue sarcoma-upreg
WO2004048938-A2.
                                                                                                                                                                      Mouse cancer ass WO2004060304-A2.
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EP806480-A2.
                                         (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.4%;
t Local Similarity 48.3%;
                                                                                                                                                                                           ADQ97107 standard;
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                                                                                                                                                                                                                                                                                                                                                                  WO2004067740-A1.
12-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                   ADR28249 standard; DNA; 59999 Human low density lipoprotein
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Tylactone synthase
EP791655-A2.
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                                                                                                                                                                                                                                                                                                           ABD33301 standard;
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ry Match
2.4%; Score 36.2; DB 2;
t Local Similarity 55.0%; Pred. No. 1.6e+02;
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ry Match 2.4%; Score
L Local Similarity 55.0%; Pred.
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genomic DNA HD17-053.
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sequence MD08-002,
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re 36.2;
1. No. 1.
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.5e+02;
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Query Match PROTEIN DES
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RESULT 862
ID BACCO
 RESULT 870
ID AAF162
DE Human 1
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RESULT 868
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                         Prokaryotic essential gene #23755. WO200277183-A2. 03-0CT-2002.
                                                                                                                                                                                                                                                                                                                                                              ABD02947 standard; DNA; 1512 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Banana gene conferring disease resistance WO2003000906-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ABD11412 standard; DNA; 894 BP.
Pseudomonas aeruginosa polynucleotide #10016
US6551795-B1.
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(SYGN) SYNGENTA PARTICIPATIONS AG.
12Y Match 2.4%; Score
1 Local Similarity 46.7%; Pred.
AAF16277 standard; cDNA; 3779
Human prostate cancer antigen
                                                                                                                                                                                             Bacterial polynucleotide US2003233675-A1.
                                                                                                                                                                                                                   ADT44558 standard; cDNA;
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Zea mays DNA fragment SEQ ID
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Zea mays DNA fragment SEQ ID
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D NO: 30530.
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Pred. No.
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WO200055174-A1.

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RESULT 877
RESULT 878
ID ADH62916 standard; DNA;
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RESULT 873
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30-DEC-1998.
(UNIW ) UNIV WASHINGTON.
(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
2.4%; Score 36;
                                                                                            ADD00956 standard; DNA;
Human Jagged 2 encoding
                                                                                                                                                        ABQ99655 standard; DNA; Human membrane spanning WO200262946-A2.
                                                                                                                                                                                                                              Human musculoskeletal system-associated US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                           AAL36491 standard; DNA; 15362 BP. Human musculoskeletal system related WO200155367-A1.
               US2003170636-A1.
                         Human Jagged
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WO2003077848-A2.
                                                                                                                                                                                                                                                ADJ30229 standard; DNA; 15362 BP.
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WO9858958-A2.
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                                                                            25-SEP-2003
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                                                                                                                                                                                                                                                                                                                                       ABX59479 standard,
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                                                            (ISIS-) ISIS
cy Match
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DNA SEQ ID
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4-domain family, subfamily A
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1.7e+02;
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2e+02;
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1.5e+02;
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PHARM INC

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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                     ACN45150 standard; DNA; 217409 BP. Human genomic sequence hCG34092. WO2003073826-A2.
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US2003207839-A1.
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                                                                                                                                                                 ADJ11721 standard; DNA; 561 BP.
Rice cDNA modulated by post-transcriptional gene
                                                                                                                                                                                                                                                                                  ACH44435 standard; cDNA; 469 B
Human foetal brain cDNA #5160.
US2003073623-A1.
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W02003073826-A2.
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Mouse genomic sequence mCG2215.
WO2003073826-A2.
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2.4%;
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Local Similarity
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BRIGGS S P.
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GLAZEBROOK J.
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KATAGIRI F.
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similarity 58.3%;
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                              MOUGHAMER T. PROVART N.
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3.1e+02;
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2e+02;
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SULT 892
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                                                                               AAZ93365 standard; DNA;
Sequence encoding F-box
WO200012679-A1.
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Rice gene, SEQ ID 3822.
WO2003000898-A1.
                        cDNA of Human F-box
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Toxicity modelling
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                WO200255665-A2.
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Rice DNA modulated
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                               AAL41056 standard;
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                                               (UYNY) UNIV NEW YORK STATE.
ry Match 2.4%;
Local Similarity 51.7%;
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ZHUT/) ZHU T.
WANG/) WANG X.
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GLAZEBROOK J.
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PROVART N.
RICKE D.
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th 2.4%; Score
Similarity 47.9%; Pred.
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KATAGIRI F.
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UNIV NEW YORK STATE.
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24-SEP-2003.
(REAS-) RES ASSOC BIOTECHNOLOGY.
22.4%; Sco
22.4%; Pre
                                                                                                                                                                                                                                                                           Human protein encoding cDNA SEQ ID WC2004009834-A2.
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EP1347046-A1.
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Novel human cDNA SEQ ID NO 408.
US2003104529-A1.
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11-OCT-2001.
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ADH76501 standard; DNA; 2572 BP.
727 amino acid human neurotransmitter transporter protein encoding
                                                                                                                      29-JAN-2004.
                                                                                                                                    Human protein encoding WO2004009834-A2.
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Human cDNA of the invention
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(TANG/) TANG Y T.
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de SEQ
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GPCR-like
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US2003219774-A1.

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(WEST/) WESTPHAL R.
(FEDE/) FEDER J N.
(LEEL/) LEE L M.
                                                                                                                                                                                          ADS10356 standard;
Human therapeutic WO2004080148-A2.
                                                                                                                                                                                                                                                           AAS72201 standard; cDNA; DNA encoding novel human WO200175067-A2.
                                                     WO2004065545-A2.
                                                                                                                        ACN40359 standard; cDNA; 361
Tumour-associated antigenic
WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                     Novel human cDNA sequence WO200281731-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ11615 standard;
Rice DNA modulated
US2003135888-A1.
                                                                         ADR25659 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                      ABX71181 standard;
                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
(GOOD/) GOODRICH F
                                                                                                                                                                         (NUVE-) NUVELO INC.
                                (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
AD36022 standard;
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GOFF S A.
KATAGIRI F.
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WANG X.
CHANG H.
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COOPER B.
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post-transcriptional
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SEQ 1
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marker #1520.
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nic target
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diagnostic
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RESULT 918
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                                                                                               ABZ32962 standard; cDNA; 174 E Human colon tumour cDNA clone WO200283070-A2.
                 Corn seedling-derived US2003237110-A9. 25-DEC-2003.
                                                                                                                                                                       ABZ33005 standard; cDNA; 174 I
Human colon tumour cDNA clone
W0200283070-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          AAA78081 standard; cDNA; 174 cDNA encoding human colon tur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ97640 standard; DNA; 79731 BP.
Mouse cancer associated sequence MD10-020, SEQ ID
                                                                                                                                                                                                                                                 Colon tumour related WO200149716-A2.
                                                                                                                                                                                                                                                                   AAI28819 standard;
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                                            ADS67683 standard;
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ry Match 2.4%;
t Local Similarity 57.1%;
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PHARM INC.
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ved polynucleotide
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ed determined
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(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                           09-AUG-2001.
(MOLE-) MOLECULAR DYNAMICS INC.
2.4%; Score
2.7%; Pred.
                                         AAI48636 standard;
                                                                                           ABA68422 standard;
Human foetal liver
WO200157277-A2.
                                                                                                                                                            AAI23315 standard; DNA
Probe #13248 for gene
WO200157278-A2.
                                                                                                                                                                                                                               AAS65914 standard;
DNA encoding novel
WO200175067-A2.
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Cotton androecium t
US2004123340-A1.
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17-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                           Human foetal brain
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(FISH/) FISHER D
(LIUJ/) LIU J.
                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                     CH45185 standard;
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MOLECULAR DYNAMICS INC.
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RESULT 934
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RESULT 929
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                                      WO200218632-A2.
                                                                                                                                                                Human genome-derived single WO200186003-A2.
                                                                                             Oligonucleotide
WO200218632-A2.
07-MAR-2002.
                                                                                                            ABQ19226 standard; DNA; 687 BP
Oligonucleotide for detecting
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                                                                                                                                                                                                                                                                                                        ABS42178 standard;
Human liver single
WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                         Human brain expressed single WO200157275-A2.
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Human breast cell;
WO200157271-A2.
                                                      ABQ19227 standard;
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ry Match 2.4%;
t Local Similarity 45.9%;
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Probe #13879 for g
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ry Match 2.4%; Score
Liccal Similarity 45.9%; Pred.
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Best Local Similarity

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Best Local Similarity
RESULT 943
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Best Local Similarity
                                                                                                                                         ABA55830 standard;
Human foetal liver
WO200157277-A2.
Human breast
                                                                          Probe #4172 used to
                                                                                     AAI35486 standard; DNA; 1969 BP.
                                                                                                                                                                                                                     Probe #4038 for gene expression analysis WO200157278-A2.
                                                                                                                                                                                                                                        AAI14105 standard; DNA; 1969
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ry Match 2.4%;
t Local Similarity 47.0%;
                                                                                                                                                                                                                                                                                              Human cDNA sequence EP1074617-A2.
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Human cDNA sequence SEQ ID NO:13081.
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CY Match 2.4%; Sc
Local Similarity 45.9%; Pr
        BA45341 standard;
                          (MOLE-) MOLECULAR DYNAMICS INC.

YY Match 2.4%; Sc.
Local Similarity 45.9%; Pr
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No. 43;
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No. 69;
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RESULT 948
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(MOLE-) MOLECULAR DYNAMICS INC.
(MOLE-) MOLECULAR DYNAMICS INC.
2.4%; Sc
ery Match
2.4%; Sc
ery Match
45.9%; Pr
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Human cell cycle and proliferation
W0200107471-A2.
01-FEB-2001.
                                                                                                                                               (INCY-) INCYTE GENOMICS INC.
ry Match 2.4%;
t Local Similarity 47.0%;
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xy Match 2.4%; Score
t Local Similarity 45.9%; Pred.
                                      ADH41892 standard; DNA; 2
Novel human nucleic acid
                                                                                                         Human NOV45f gen
WO2003076642-A2.
                                                                                                                             ADE47789 standard;
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19-AUG-2001.
(MOLE-) MOLECULAR DYNAMICS INC.
2.4%; Score
45.9%; Pred.
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Probe #3949 used to measure gene
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LY Match 2.4%; Score

L Local Similarity 45.9%; Pred.
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t Local Similarity 45.9%; Pr
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Similarity 45.9%;
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expressed single
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exon probe, SEQ
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Best Local Similarity
RESULT 956
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Bacterial polynucleotide US2003233675-A1.
                                                   AAC48435 standard; DNA; 2173 BP. Arabidopsis thaliana DNA fragment EP1033405-A2.
                                                                                                      ADO54827 standard; DNA; 2136 Human macrophage stimulating KR2003003840-A.
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(ZHON/)
(CASM/)
                                 Local Similarity
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CATTERTON E.
SHENOY S G.
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AGEE M L.
CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
GANGOLLI E A.
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PATTURAJAN I
KEKUDA R.
MILLER C E.
RIEGER D K.
PENA C B A.
SHIMKETS R
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SPADERNA S
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BURGESS C E.
KHRAMTSOV N V.
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VERNET C A M.
LEITE M W.
GUO X S.
ANDERSON D W.
SPYTER K A.
CERTACH Y
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ZHONG M.
CASMAN S J.
VOSS E Z.
BOLDOG F L.
PADIGARU M.
SMITHSON G.
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Best Local Similarity
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ABV94342 standard; cDNA; 2219 BP.
Breast carcinoma related nucleotide sequence
                                                                                     AAT62437 standard;
Human L5/3 partial
                                                                                                                                                                  AAT62436 standard;
Human L5/3 partial
US5606029-A.
                                                                                                                                                                                                                                                  AAQ79723 standard; cDNA to mRNA; 2219 BP. Human L5/3 tumour suppressor gene (Cys214 US5315000-A.
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10-DEC-1998.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                              (CHIL-)
                                                                                                                                                       25-FEB-1997
                                                                                                                                                                                                         (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
ry Match 2.4%; Score 35.6;
t Local Similarity 57.0%; Pred. No. 73
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EP750040-A2.
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Macrophage stimulating protein C672 deletion
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2.4%; Score 35.6;
Similarity 57.0%; Pred. No. 73;
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Score 35.6; I
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Pred. No. 73;
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                                                                                                                                                                                                               ACN41133 standard; cDNA; 2493 BP. William diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ WO200153312-A1.
                                                                                                                                                                                                   Human diagnostic WO2004023973-A2.
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Human tumour-associated;
WO2004060270-A2
                                       WO2003018612-A2.
                                                            Human extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC42371 standard; DNA; 2440 BP
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US5606029-A.
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                                                                             ACC42370 standard; DNA; 2573
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CY Match 2.4%;
Local Similarity 57.0%;
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Leukaemia-related DNA sequence
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                                                                                                                                          (INCY-) INCYTE
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                                                                                                                                                                                                                                                                                                                        HYSE-) HYSEQ INC.
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N/) KERN W.
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2.4%;
Y 57.0%;
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                                                        messenger,
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ID NO 1719.
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; Score 35.6; I
; Pred. No. 74;
                                       3 BP.
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No. 78;
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No. 74;
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RESULT 976
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07-FEB-2001.
(HELI-) HELIX RES INST.
(HELI-) 2.4%; (
Match 2-4ty 47.0%;
                                                      Human tumour suppressor mRNA & W02003058201-A2.
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BP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                   AAH17866 standard; cDNA;
Human cDNA sequence SEQ 1
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                                  (QUAR-) QUARK BIOTECH INC.
                                                                                                                             WO200175067-A2.
11-OCT-2001.
                                                                                                                                              DNA encoding novel
                                                                                                                                                                                                            Human diagnostic WO2004023973-A2.
                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                       AAS65913 standard;
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WO2003018612-A2.
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ry Match 2.4%;
t Local Similarity 57.0%;
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standard; DNA; 15377 BP.
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human diagnostic
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nd therapeutic
                  2.4%;
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er, EXMES-14,
                  Score 35.6;
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1.3e+02;
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RESULT 990
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                                                                                                                     ABD32827 standard; DNA; 129381 BP. Human cancer-associated genomic DN W02004074320-A2.
                                  WO2004060304-A2.
                                         ADQ97526 standard; DNA; 151052 BP.
Mouse cancer associated sequence MD09-009,
                                                                                                             02-SEP-2004
                                                                                                                                                                (SAGR-) SAGRES DISCOVERY.
ry Match 2.4%;
t Local Similarity 54.6%;
                                                                                                                                                                                                             ACN44586 standard; DNA; 118931 BP. Human genomic sequence hCG30014. WO2003073826-A2.
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Murine cancer-associated (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer associated WO2004060304-A2. 22-JUL-2004.
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Human cancer-associated genomi
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cy Match 2.4%;
Local Similarity 57.0%;
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ry Match 2.4%;
t Local Similarity 46.7%;
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gene MD07-119.
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No. 5.3e+02;
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No. 5.
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No. 4.7e+02;
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No. 3.4e+02;
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1.5e+02;
                                                                                                                                                                                                                                                        1e+02
                                                                                                                                                                                                                                                                                        .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
.9e+02;
                                                                                                                                                                                                                                                                                                   DB 10;
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                                            SEQ
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 12;
                                            IJ
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Length 151052;
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                                                                                     129381;
                                                                                                                                                                                                                                                                                                   110000
                                                                                                                                                                                                                                                                                                                                  92219;
                                                                                                                                                                                                                                                                                                                                                                                                                        86149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49087;
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SBBB

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Query Match
Best Local Similarity
RESULT 1001
                                                                                                                                                Best Local Similarity RESULT 1000
                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 999
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RESULT 996
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RESULT 995
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                                                                                         ABX37512 standard; cDNA; 428
Bovine EST associated with 1
US2002137139-A1.
26-SEP-2002.
(BYATY) BYATT J C.
ADR46439 standard; DNA; B napus caltractin-like WO2004070035-A2.
                                                            (MATH/) MATHIALAGAN (TAON/) TAO N. (WARR/) WARREN W C.
                                                                                                                                                                                      Pseudomonas aeruginosa polynucleotide US6551795-B1. 22-APR-2003.
                                                                                                                                                                                                                     ABD11421 standard; DNA; 423
                                                                                                                                                                                                                                                                                                       ABX36854 standard; cDNA; 41
Bovine EST associated with
US2002137139-A1.
26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABX42580 standard; cDNA; 41 Bovine EST associated with US2002137139-A1.
                                                                                                                                                                               (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS90684 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX38848 standard; cDNA; 38
Bovine EST associated with
US2002137139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK83568 standard; DNA; 201143 Human DNA differentially expres WO200228999-A2.
                                                                                                                                                                                                                                                                         (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN
(TAON/) TAO N.
                                                                                                                                                                                                                                                                                                                                                                             (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                 (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WARR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2002.
(GENE-) GENE LOGIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BYAT/)
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                                                                                                                                                                           GENOME THERAPEUTICS
                                                                                                                                                                                                                                                             WARREN W C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BYATT J C.
MATHIALAGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA;
human
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2.4%;
54.6%;
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                                         2.4%;
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          428 BP.
protein
                                                                                                                        428 BP.
th lactation/muscle/fat
                                                                                                                                                                                                                                                                                                                          416 BP.
th lactation/muscle/fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201143 BP. expressed
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diagnostic
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th lactation/muscle/fat
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lactation/muscle/fat
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Pred.
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         coding
                                         35.4;
No. 37;
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No. 36;
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No. 36;
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          sequence
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.8e+02;
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          SEQ
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          NO:
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Best Local Similarity RESULT 1002
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BA
            RESULT 1009
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                                                                                                                            Best Local Similarity RESULT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1005
                                                                                                                                                    Query Match
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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA69809 standard; DNA; 579 Rice gene, SEQ ID 3132. WC2003000898-A1.
                                                                                                    ADQ85345 standard; cDNA; 1525 BP.
Human tumour-associated antigenic target (TAT) cDNA sequence #2159
                                                                                                                                                                                                           ADQ83950 standard; cDNA; Human tumour-associated a WO2004060270-A2.
                                                                                                                                                                                                                                                      (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.

ry Match
2.4%; Score 35.4;
Local Similarity 49.2%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                M lichenicola melithiazol synthesis
                                                                                                                                                                                                                                                                                                                                                                                                  Human BSK-36-8 complementary strand EP1310567-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         ADE76270 standard; DNA; 701 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACH14525 standard; cDNA; 492
Human adult brain cDNA #1737.
US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX35170 standard; cDNA; 450 BP.
Bovine EST associated with lactation/muscle/fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2004
ACF34491 standard; DNA; 1526
                                                                                                                                                            (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                             ACF04830 standard; DNA;
                                             (GETH ) GENENTECH INC.
(WUTD/) WU T D.
(ZHOU/) ZHOU Y.
                                                                                            O2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                    local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 2.4%; occal Similarity 48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r/) BYATT J C.
H/) MATHIALAGAN |
N/) TAO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNGENTA PARTICIPATIONS AG.

2.4%; Score 35.4;

Similarity 48.3%; Pred. No. 43
                                                                                                                                                                                                                                                                                                                                                                           OLIGENE GMBH.
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                     Similarity
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                     2.4%;
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48.7%;
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Pred.
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Pred.
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                       Pred.
                                Score
                                                                                                                                                                                                                       target (TAT)
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No. 39
                                                                                                                                                                                                                                                                                                                                                    35.4;
No. 47
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No. 37;
                     35.4;
No. 69
                                                                                                                                       35.4;
No. 69;
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No. 38;
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Query Match
Best Local Similarity
RESULT 1017
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RESULT 1014
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Best Local Similarity
RESULT 1010
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15-APR-2004.
(GETH) GENENTECH INC.
(GETH) GENENTECH INC.
2.4%; (
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16-JAN-2003.
(MILL-) MILLENIUM PHARM INC.
2:ry Match
2:4%;
47.2%;
                                                                                                                                                                                                      ACN92807 standard; DNA; 3535 |
Breast cancer related marker,
US2003099974-A1.
                                 Human dithp int WO200297031-A2.
                                                                                                                        ADI24476 standard; cDNA; 3718 Human modifier of Chk1 (MCHK) W02004004785-A1.
                                                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC.
PLY Match 2.4%;
It Local Similarity 52.3%;
                                                                                                                                                                                                                                                                                                          ACA39654 standard; DNA; 1770 BP. Prokaryotic essential gene #21311. WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    AAT91855 standard; cDNA; 1559 DUB-1 enhancer/promoter. W09706247-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACC50093 standard; cDNA; Breast cancer associated WO2003004989-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene encoding angiogenesis
                                                         ACC46250 standard;
                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
ry Match 2.4%;
t Local Similarity 47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF81420 standard; DNA; 1526 BP.
Leukaemia-related DNA sequence #1976.
                                                                                                    (EXEL-) EXELIXIS INC.
                                                                                                                15-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACN39732 standard; cDNA; 1526 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
(UYLU-) UNIV LUDWIG MAXIMILIANS.
(HAFE/) HAFERLACH T.
                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
                                                                                                                                                                                                                                                                                                                                                        DANA FARBER CANCER INST INC.
th 2.4%; Score 3
Similarity 51.6%; Pred. N
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KERN W.
          INCYTE
                                           ındard; cDNA; 3978
intracellular sigr
 GENOMICS
2.
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No. 74;
 35.4;
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                                            protein-encoding
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                                                                              DB 12;
.1e+02;
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В
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                                                                                                                                     SEQ
                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA325923,
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                                                                                                                                     IJ
Length 3978;
                                                                                                                                                                                                                                                                                                                                                                    Length 1559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                          Length 1770;
                                                                                      Length
                                                                                                                                                                                  Length 3535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1526;
                                                                                                                                      NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:4063.
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Best Local Similarity RESULT 1025
                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 1024
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1019
                                                                                                      Query
                                                                                                                                                                                             Query Match
                                                                                                                                                                         WO2004-0-07-NOV-2002.
(ISIS-) ISIS PHARM INC.
2.4%;
Match 2-1ty 53.2%;
                                                        ABD32684 standard; DNA; Human cancer-associated
                                              WO2004074320-A2.
                                                                                                                                    ADQ97945 standard; DNA; 39414 BP. Mouse cancer associated sequence WO2004060304-A2.
                                                                                                                                                                                                                                      AAD52172 standard; DNA; 26000 BP. Human interferon gamma receptor 1
                                                                                                                                                                                                                                                                                                                                                                                                           ABD32919 standard; cDNA; 5186 BP. Human cancer-associated cDNA HR18-043.8. W02004074320-A2.
                                                                                                                                                                                                                                                                                                                      Human cancer-associated WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                            ABD33393 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD32918 standard; cDNA; 5099 BP. Human cancer-associated cDNA HR18-043.7. WO2004074320-A2.
                                                                                                                (SAGR-) SAGRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer-associated cDNA HR18-043.9. WO2004074320-A2.
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ry Match 2.4%;
t Local Similarity 59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP11018622-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse male enhanced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY INC.
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ch 2.4%;
l Similarity 46.2%;
                      SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                SAGRES DISCOVERY INC. h 2.4%; Similarity 59.7%;
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                                                                                                               DISCOVERY INC.
                                                                                        2.4%;
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lantigen 2
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 2.4%;
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                                                      41991 BP.
genomic DNA
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No. 2.
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                                                                                        35.4;
No. 3.
                                                                                                                                                                                                                                       (IFNGR1)
35.4; DB 13;
No. 3.6e+02;
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No. 1.
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No. 2.7e+02;
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No. 1.
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No. 1.3e+02;
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No. 1.
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                                                                                        DB 12;
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.8e+02;
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.2e+02;
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.2e+02;
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.2e+02;
                                                                                                                                               SEQ ID
         Length 41991;
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                                                                                                   Length 39414;
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Query Match
Best Local S
RESULT 1030
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Best Local Similarity
RESULT 1034
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ID ACF0481
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                                                                                                     Query Match
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                                                   AUG:/U184 standard; DNA; 379652
DNA of BAC bA236m15-00303.
                                                                                                                                    ABX16390 standard; DNA; 6 Mouse high growth region. US2002155564-A1.
                                  03-JAN-2003
                                                                                                                                                                                                                           Murine carcinoma
US2004072154-A1.
15-APR-2004.
                                                                                                                                                                                                                                                                                                                  30-JAN-2003
                                                                                                                                                                                                                                                                                                                             Mouse Fish gene.
WO2003008583-A2.
                                                                                                                                                                                                      (ENGE/) ENGELHARD
                                                                                                                                                                                                                                                                                                                                                   ADB72545 standard; DNA; 96597
                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               ADA02807 standard; DNA; 96597 BP. Mouse Fish carcinoma associated c
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAGR-) SAGRES DISCOVERY.

ry Match 2.4%;
t Local Similarity 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine cancer-associated (CA) W02004058146-A2.
                                                                                                                                                                                                                                                            1DM74402 standard; DNA;
                                                                                                                                                                                                                                                                                                          (SAGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse Fish genomic WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC85287 standard;
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ry Match
2.4%;
t Local Similarity 47.5%;
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                                                                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY.
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(SAGR-) SAGRES DISCOVERY INC.
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ry Match
2.4%; Score 35.4;
Liocal Similarity 49.2%; Pred. No. 46
                                                                                                                                                                                                                MORR/) MORRIS D W.
                                                                                                                                                                                                                                                                                 ocal Similarity
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                                                                                                            ) UNIV CALIFORNIA.
                      ISIS INNOVATIONS LTD.
                                                                                                                                                                                                                                                                               SAGRES DISCOVERY.
h 2.4%;
Similarity 51.6%;
                                                                                                                                                                                                                                                d; DNA; 96597 associated (C
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                                                                                                                                                         DNA; 659158
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2.4%;
47.2%;
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Score
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cluster.
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                                                                                                                                                          BP.
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35.4; DB 10;
No. 5.8e+02;
                                                                                       35.4;
No. 5.
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No. 5.
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No. 5.
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No. 5.
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No. 5.
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5 -
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5
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5.8e+02;
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4e+02;
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.4e+02;
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.1e+02;
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Query Match
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RESULT 1037
                              BREI
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RESULT 1043
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RESULT 1039
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Best I
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22_JUL_2004.
22_JUL_2004.
(SAGR-) SAGRES DISCOVERY INC.
2.4%;
ery Match 2.4%;
50.9%;
                                                                                                                Rice gene conferring WO2003000906-A2.
                                      Thale cress cDNA repressed WO2004035798-A2.
                                                           ADN73638 standard; cDNA;
                                                                                                                          ADA48417 standard; DNA; 500 BP.
Rice gene conferring disease resistance
                                                                                                                                                                                                                                                             (GENE LOGIC INC. 2.4%; ry Match 2.4%; t Local Similarity 63.5%;
                                                                                                                                                                                                                                                                                                        WO200228999-A2.
                                                                                                                                                                                                                                                                                                                ABK83573 standard; cDNA; 130263 BP.
Human cDNA differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                         ADP80536 standard; DNA; 118788
Human HPC2/ELAC2 gene SeqID1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABD32886 standard; DNA; Mouse cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer-associated genomic WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD32911 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ97050 standard;
                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG

CY Match 2.4%; Score

Local Similarity 48.1%; Pred.
                                                                                                                                                                                                                           US2002137139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-SEP-2004
                                                                                                                                                                                                                                              ABX39880 standard;
                                                                                                                                                                                                                                                                                                                                                                 (TAKA/) TAKAHASHI H.
(WATA/) WATANABE M.
(FURU/) FURUSATO M.
(HONS ) YAKULT HONSHA
                                                                                                                                                                                                                                                                                               1-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                       BYAT/) BYATT J C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAGR-) SAGRES DISCOVERY INC.
 Local Similarity
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Local Similarity 55.2%;
                                                                                                                                                                          WARREN W C.
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                   CROPDESIGN
                                                                                                                                                                                                                                    associated
                   Ž.
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2.4%;
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2.4%;
46.2%;
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genomic DNA
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th lactation/muscle/fat
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 No. 46;
                                                                            35.2;
No. 45;
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No. 6e+02;
                                                                                                                                                        35.2;
No. 41;
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No. 6e
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No. 5.
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No. 5.
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                                                                                                                                                                                                                                                                 6.4; DB 6;
0. 6.3e+02;
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6e+02;
                                               expressing
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.8e+02;
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.8e+02;
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.8e+02;
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                                                                                                                                                                           ABK62083 standard; cDNA; 1010 BP. Human cDNA encoding novel secreted W0200214358-A2.
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Arabidopsis thaliana
EP1033405-A2.
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                                                                                              AAF61042 standard; DNA; 2250 P. putida KT2440-associated I DE19935088-A1.
                                                                                                                                                                                                                                                       ACL20017 standard; DNA; 708 BP. DNA clone originating in barley W02003057877-A1.
                                                                                                                                                                                                                                                                                                                                     ACL20023 standard; DNA; 6
DNA clone originating in
WO2003057877-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADC75910 standard; DNA; DNA homologous to phytop WO2003020905-A2.
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  ADA02845
                                  (TIGR-) TIGR INST GENOMIC RES.
(QUIA-) QUIAGEN GMBH.
(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
(MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
                                                                                                                                                        (ELIL ) LILLY & CO
                                                                                                                                                                    21-FEB-2002
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ry Match 2.4%;
t Local Similarity 53.7%;
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                  35.2;
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RESULT 1057
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US2004072154-A1.
15-APR-2004.
(MORR/) MORRIS D W.
                                                                                                                                       ADB72582 standard;
Mouse Fgfr3 mRNA.
WO2003008583-A2.
                                                                                                                                                                                                                                                                               HOMO protein encoding WO2004014946-A1.
19-FEB-2004.
(NEWO-) NEWORGEN LTD.
                                                           Mouse Fgfr3 genomic WO2003045230-A2.
                                                                               ADC85323 standard;
                                                                                                                                                                                                                       Mouse Fgfr3 carcinoma associated cDNA, WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                 AAZ09484 standard; DNA; 2606 Bovine retina Ih ion channel W09942574-A1.
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30-JAN-2003.
(SAGR-) SAGRES DISCOVERY.
2.4%;
2.4%;
30-JAN-2003.
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Mouse Fgfr3 cDNA.
WO2003008583-A2.
                                                                                                                                                                                          (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                          ADA02844 standard; cDNA; 2887
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WO2003045230-A2.
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Similarity 51.2%;
                 SAGRES DISCOVERY.

1.4%;
Similarity 51.2%;
 standard;
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c sequence.
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57.1%;
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DNA fragment.
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Best Local Similarity
RESULT 1071
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Query Match
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RESULT 1065
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                                                                                                 tcp gene cluster.
                            ACN44380 standard; DNA; 76846 BP.
Mouse genomic sequence mCG18525.
WQ2003073826-A2.
12-SEP-2003.
                                                                                                           ADS73531 standard; cDNA; 73882 BP.
                                                                                                                                                                      Human genomic sew
WO2003073826-A2.
                                                                                                                                                                                                                                                                                           ADR66967 standard; DNA; 34571 Mouse cancer associated gene
                                                                                                                                                                                           ACN44230 standard;
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Mouse fibroblast growth f
US6265632-B1.
24-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL20581 standard; DNA; 3318 BP. Drosophila melanogaster genomic W0200171042-A2.
                     (SAGR-) SAGRES DISCOVERY.
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US2004072154-A1.
15-APR-2004.
                                                                                                                                                                                                                                                                                 #O2004074321-A2.
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Bovine retina Ih ion
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                                                                                                                                                                                                                                                                                                                                             EPIGENOMICS AG.
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ENGELHARD E
                                                                                                                                                                              dard; DNA; 66973 BP. sequence hCG21559.
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35.2; DB 11;
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.2e+02;
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.le+02;
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.7e+02;
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.8e+02;
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,4e+02;
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.7e+02;
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.1e+02;
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2e+02;
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Maize gene conferring disease resistance in
WO2003000906-A2.
                                Human foetal bra
US2003073623-A1.
                                                                                               Human soft tissue sarcoma-upregulated W02004048938-A2.
                                                                                                                ADQ19577 standard; DNA, 393
                                                                                                                                                                                         JS2002137139-A1.
                                                                                                                                                                                                 Bovine EST associated with
                                                                                                                                                                                                        ABX40527 standard; cDNA;
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Human GPCR gene SEQ ID NO:1369.
                                                ACH44942 standard; cDNA; 487 BP.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA58686 standard; cDNA;
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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FISH/) FISHER D K.
LIUJ/) LIU J.
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DRMANAC R T.
LABAT I.
STACHE-CRAIN B.
                                                               PROTEIN DESIGN LABS h 2.4%; Similarity 50.3%;
                                        brain cDNA #5667.
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EST #185.
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EST #330.
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th lactation/muscle/fat
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Best Local Similarity
RESULT 1087
ID ABD08729 standard; I
DE Pseudomonas aeruginc
PN US6551795-B1.
PD 22-APR-2003.
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RESULT 1084
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RESULT 1082
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Best Local Similarity
RESULT:1080
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RESULT 1083
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ESULT 1085
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                                                                                               ADM47892 standard; DNA; Polynucleotide sequence US2003233670-A1.
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Rice gene, SEQ ID 2054.
WC2003000898-A1.
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(RANK/) RANK D R.
(HANZ/) HANZEL D F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1074617-A2.
07-FEB-2001.
                                                                                                                                                                         ADP28033 standard; DNA; 1176 BP. Human secreted protein encoding WO2004055732-A2.
29-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding novel WO200166689-A2.
                           ABD08729 standard; DNA; 1488
                                                                                                                                                                                                                                                                                                              ADT43885 standard; cDNA; 870 BP. Bacterial polynucleotide #18636.
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                                                                (EDGE/) EDGERTON M
(CHOM/) CHOMET P S.
(LACC/) LACCETTI L
                                                                                                                                                                                                                                                                                                      US2003233675-A1.
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                                                                                                                                                               (FIVE-) FIVE PRIME
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(SLAT/) SLATER S
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                 andard; DNA; 1488 BP.
aeruginosa polynucleotide #7333.
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Best Local Similarity
RESULT 1092
ID ADP28010 standard; D
DB Human secreted prote
PN W02004035732-A2.
PD 29-APR-2004.
ID
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PN
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US6551795-B1.
22-APR-2003.
                                                    (ZERH/)
(PATT/)
(KEKU/)
                                                                                      ADJ79057 standard;
Human NOVX protein
US2004014053-A1.
                                                                                                                                                    Novel human nucleic WO2003102159-A2.
                                                                                                                                                                                                                                     ADE47787 standard; DNA
Human NOV45e gene SEQ
WO2003076642-A2.
                                                                                                                                                                                                                                                                                                                                                                                   Human secreted p WO2004035732-A2.
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Human cDNA differentially expressed in a liver
US2003108871-A1.
                                                                                                                                                                               ADH41894 standard; DNA;
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Human polynucleotide
WO200164835-A2.
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(CURA-) CURAGEN CORP.
                  MIHS.
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ry Match 2.4%; Score
c Local Similarity 50.3%; Pred.
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PATTURAJAN M.
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MILLER C E.
RIEGER D K.
PENA C E A.
SHIMKETS R A.
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protein encoding
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protein encoding sequence
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Nov45E
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SEQ ID NO:149.
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d NOV36b.
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RESULT 1099
ID ABS5933
DE Human m
PN WO20023
PD 25-APR-
                       Best Local Similarity
RESULT 1100
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Best Local Similarity
RESULT 1096
                                       Query Match
                                                                                                   Query Match
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                                                     ABS59330 standard; DNA; 2011
Human macrophage stimulating
WO200233087-A2.
25-APR-2002.
ADJ38433 standard; cDNA; Human cDNA encoding prote US2003212256-A1.
                                                                                                                                 ABT08324 standard; DNA; 2011 Human NOV7 gene sequence.
                                                                                                                                                                                      Human equine herpesvirus p24 homologue-encoding W0200157188-A2.
                                                                                                                 13-JUN-2002
                                                                                                                         Human NOV7 gene WO200246408-A2.
                                                                                                                                                                                                                                                         AAH17389 standard; cDNA; 1851 BP.
Human cDNA sequence SEQ ID NO:16827.
                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                      ABA08292 standard; cDNA; 1890 BP
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(KHRA/
(ORTT/
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(CASM/)
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ROTHENBERG
SPADERNA S
HJALT T.
                                                                                                          CURAGEN CORP.
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CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
GANGOLLI E A.
                                              CURAGEN CORP.
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RASTELLI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                               GERLACH V.
BURGESS C E.
KHRAMTSOV N
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CASMAN S J.
VOSS E Z.
BOLDOG F L.
PADIGARU M.
SMITHSON G.
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ANDERSON D
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VERNET C !
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      cDNA; 2011 BP.
protein NOV5.
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                                                                    precursor-like
                              DB 6;
le+02;
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99;
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98;
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94;
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le+02;
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                                                                    gene.
                                                                                                                                                                1890;
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RESULT
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PN WO
                                                    Best Local Similarity
RESULT 1106
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Best Local Similarity
RESULT 1103
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RESULT 1101
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(COLD/) GOLDMAN B S.
                                                                                                                                                     AAD26582 standard; cDNA; 2200 BP. Human MSP precursor-like protein, POLY13 encoding WO200185767-A2.
                                                                                                                                                                                                                                                                                                       ABK92064 standard; DNA; 2200 EDNA encoding novel hepatoctye WO200229058-A2.
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WO200229058-A2.
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ADE47779 standard; DNA; ;
Human NOV45a gene SEQ ID
WO2003076642-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT43313 standard; cDNA; 2139 BP.
Bacterial polynucleotide #18064.
US2003233675-A1.
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                                                                                                                                     5-NOV-2001
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SPYTEK K A.
GANGOLLI E A.
FERNANDES E R.
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GUNTHER E.
ELLERMAN K.
SHIMKETS R A.
PADIGARU M.
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GERLACH V.
MACDOUGALL J R.
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BURGESS C E.
ZERHUSEN B D.
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PEYMAN J A.
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56.5%;
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56.5%;
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D NO:141.
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                                                                          DB 6;
1.1e+02;
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1.1e+02;
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1.1e+02;
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1.1e+02;
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1e+02;
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le+02;
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Query Match
Best Local Similarity
RESULT 1110
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Best Local Similarity
RESULT 1109
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Best Local Similarity
RESULT 1107
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                                     AAS83814 standard;
DNA encoding novel
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                Human NOVX protein Nov45A gene sequence.
U$2004014053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003102159-A2.
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ACN41132 standard; cDNA; 2533 BP
                         (HYSE-) HYSEQ
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                                                                              (SHEN/)
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(PATT/)
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CATTERTON E.
SHENOY S G.
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RASTELLI L.
AGEE M L.
CHAUDHURI A.
CHAUT J S.
DIPIPPO V A.
EDINGER S R.
BISEN A J.
GANGOLLI E A.
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BURGESS C E.
KHRAMTSOV N V.
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ZHONG M.
ZHONG M.
CASMAN S J.
VOSS E Z.
BOLLDOG F L.
PADIGARU M.
SMITHSON G.
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MILLER C E.
RIEGER D K.
PENA C E A.
SHIMKETS R A.
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SPADERNA S
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PATTURAJAN
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VERNET C I
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SPYTEK K A.
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No.
                                             protein #19618
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1.1e+02;
                                                                DB 12;
1.1e+02;
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1.1e+02;
             1.1e+02;
                    DB 5;
                   Length
                                                                      Length 2200;
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RESULT 1117
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                                                                                                                                                                                                                                                                                                                                                                                                          ADK18363 standard;
Human NOVX protein
WO2003057854-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ25501 standard; DNA; 2768 BP. Human soft tissue sarcoma-upregulated WO2004048938-A2.
ADC86968 standard; I
Human GPCR gene SEQ
EP1270724-A2.
                                                                                                                                                                                            Human NOVX protein WO2003057854-A2.
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Human NOVX protein
WO2003057854-A2.
                                                                                                                                                                                                                                                                                            T 1115
                                                                                                                                                                                                                                                                                                                                       DNA encoding novel WO200175067-A2.
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                                                                                                                                ADP13461 standard; DNA; 6008 BP.
Renal cell carcinoma differentially expressed
                                                                                                                        WO2004048933-A2.
                                                                                                                                                                                                             ADK18367 standard;
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Y Match 2.4%;
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                                                DORNER A.
STOVER J A.
SLONI D K.
                                                                           TWINE N C.

BURCZYNSKI |

TREPICCHIO
                                 Similarity
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encoding
        DNA; 6269 BP.
Q ID NO:1421.
                                                                             Σ 3
                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                         DNA; 5780 BP. encoding gene
                                                                                                                                                                                                                                                                                                                                               cDNA; 5635 BP.
human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                 encoding gene #9.
                                                                                                                                                                                                     encoding
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1.7e+02;
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1.7e+02;
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1.6e+02;
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1.4e+02;
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1.1e+02;
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Best Local
RESULT 1120
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RESULT 1126
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RESULT 1127
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RESULT 1123
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Best Local Similarity
RESULT 1119
ID AALO5754 standard;
                                     Mouse genomic sequence mCG22056. W02003073826-A2.
                                                                                                                                                                              Human nervous system WO200159063-A2.
                                                                                                                                                                                                                                                                                     AAL05755 standard; DNA; 16579 BP. Human reproductive system related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB52723 standard; DNA; 6957 BP. Primary rat hepatocyte toxicity W02003065993-A2.
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xy. Match 2.4%;
t Local Similarity 59.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GPCR gene SEQ EP1270724-A2.
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(ADSC.) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
2.4%; SCORE 35, DB 10; I
1t Local Similarity 46.8%; Pred. No. 1.8e+02;
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(ECOP-) ECOPIA BIOSCIENCES INC.
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WO2004065401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC86850 standard; DNA; 8360 BP.
Human GPCR gene SEQ ID NO:1303.
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Human nervous system related
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                      SAGRES DISCOVERY
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em related poly
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e ORF11, SEQ ID
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4.1e+02;
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2.3e+02;
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3.5e+02;
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2.9e+02;
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DB 10; Length 8360;
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Best Local Similarity
RESULT 1129
ID ACN44064 standard; D
DE Mouse genomic sequen
PN W02003073826-A2.
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ID AD
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PN US
PD 27
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                           ADN30326 standard; DNA; 121434 BP. Human Notch2 genomic DNA region #1 US2004101487-A1.
27-MAY-2004.
                                                                                                                    Murine carcinoma
US2004072154-A1.
                                                                                                                             ADM74342 standard; DNA; 96599 Murine carcinoma associated (C
                                                                                                                                                                                                                                                                    ADB72485 standard; DNA; 96599 Mouse Irf2 gene. WC2003008583-A2.
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                                                                                                                                                                                           Mouse Irf2 genomic WO2003045230-A2.
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09-AUG-2001.
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ry Match 2.4%;
Local Similarity 54.2%;
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ENGE/) ENGELHARD E
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DB 12;
7.8e+02;
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5.4e+02;
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5.6e+02;
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4.4e+02;
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7e+02;
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RESULT 1138
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                                                                                                                              ABX56967 standard; DNA;
Arabidopsis thaliana pol
US2002040489-A1.
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W02004060304-A2.
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                                                                                                                                                                                        (GEST ) GENSET.
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ry Match 2.4%;
t Local Similarity 30.6%;
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ry Match 2.4%;
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GARCIA C A.
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PRICE J L.
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h 2.3%; Score
Similarity 48.9%; Pred.
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                                                                                                                                                                     No. 60;
                                                                                                                                                                                                                                            34.8; I
No. 53;
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No.
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1e+03;
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9e+02;
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8.8e+02;
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8.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                           215126;
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ESULT 1151
                                                                                                                                                                                                      Best Local Similarian RESULT 1149
ID AAI70982 standard;
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Best Local S
RESULT 1146
                                                                                                                                             Best Local Similarity RESULT 1150
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Best Local Similarity
RESULT 1145
                                                                             Query Match
Best Local /
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                                                                     03.JAN-2003.
03.JAN-2003.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
317 Match
2.3%; Score
317 Admilarity 48.9%; Pred.
                                              AAX90405 standard; DNA; 1375
Actinomadura sp. DSM43186 35
                                                                                                               ADA49077 standard; DNA; 1290 BP. Wheat gene conferring disease re W02003000906-A2.
                                                                                                                                                                                            WO200192485-A1.
                                                                                                                                                                                                   Rat histamine H4 receptor
                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide W0200171042-A2.
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID EP1033405-A2.
                                                                                                                                                                                                                                                                                                                           06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                       AAC39827 standard;
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(INCY-) INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL12630 standard; cDNA; 6 Human steroid-induced C3A
                                                                                                                                                                       ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                      ABL13473 standard; cDNA; 935 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant cDNA #3637.
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 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .DJ42637 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    GOFF S A.

KATAGIRI F.

KREPS J.

PROVART N.

RICKE D.
ROEHM ENZYME FINLAND OY.
h 2.3%; Score
Similarity 49.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                                                                                                                                                                                                                                                                                                                             ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORP
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eceptor cDNA.
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liver cell
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Pred.
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Pred.
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                                               xylanase
 34.8; No. 96;
                                                                          34.8; I
No. 93;
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No. 89;
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No. 80;
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No. 71;
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No. 71;
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No. 69;
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No. 62;
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                                                                                                                                                                                                                                                                                                                 751;
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Best Local Similarity
RESULT 1160

ID ADT45909 standard; c
DE Bacterial polynucleo
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1152
ID AAT64930 standard; DNA; 1375
                                                                                                                                                                             Best Local Similarity
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RESULT 1153
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                                                                                                                 DNA encoding novel W0200175067-A2. 11-OCT-2001. (Hyse-) HyseQ INC.
                            Bacterial polynucleotide US2003233675-A1.
18-DEC-2003.
                                                                                                                                                                                                            Human cDNA encoding clone SMINT2
EP1308459-A2.
07-MAY-2003.
(HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                 AAS83500 standard;
                                                                                                                                                                                                                                                                                                                                ACA27342 standard; DNA; 2028 BP. Prokaryotic essential gene #8999. W0200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel W0200175067-A2. 11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-2004.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

123 SCORE 34.8;

2.3 SCORE 34.8;

2.3 Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prokaryotic essential gene #9062.
W0200277183-A2.
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21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
2.3%;
ery Match
2.3%;
57.3%;
                                                                                                                                                                                                                                                            ADB63067 standard; cDNA; 2077 BP.
Human cDNA encoding clone SMINT20007470
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                                                                                                                                                                                                                                                                                                                       (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS68016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO35997 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein cDNA sequence WO200055199-A1.
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WO9727306-A1
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CAO Y.
HINKLE
SLATER
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2.3%;
49.5%;
                                                                                                                                                      human
                                                                                                                                                                 CDNA;
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60.6%;
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human diagnostic
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diagnostic
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Pred.
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(AM35) xylanase encoding
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No. 1.3e+02;
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No. 1
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.2e+02;
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.2e+02;
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.1e+02;
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.1e+
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+02;
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Best Local Similarity
RESULT 1161
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RESULT 1167
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Best I
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06-MAY 1999.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
2:3*; Score 34.8;
3:7 Match 2:3*; Pred. No. 1.
                                                                                                                                                                                                                                                                                 (CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                          Bacterial polynucleotide US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prokaryotic essential gene #33243
WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS56030 standard; DNA; 2679 Salmonella typhi DNA for cell WO200170955-A2.
                                                                                                                        ABA15504 standard; DNA; 4034 Human nervous system related W0200159063-A2.
                                                                                                                                                                                                         AAX37250 standard; DNA; 3658
Human 3-OST-4 encoding DNA.
WO9922005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   ACF04819 standard; DNA; 3153 BP. M lichenicola melithiazol synthesis W02003080828-A2.
                                        Human nervous system WO200159063-A2.
                                                 ABA16206 standard; DNA; 4034 Human nervous system related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ23911 standard; DNA;
Human 3OST4 polypeptide
WO200292849-A2.
                                                                                                                                                                                                                                                                                                                                                                           (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.
ry Match 2.3%; Score 34.8;
Local Similarity 50.6%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASTR ) ASTRAZENECA AB.

(ASTR ) ASTRAZENECA UK LTD.

ry Match
Local Similarity 53.7%;
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                                                                              Local Similarity
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                                                                                           Match
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h 2.3%;
Similarity 58.8%;
                                                                                                    HUMAN GENOME SCI INC.
 Similarity
                    HUMAN GENOME
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58.8%;
SCI INC.
2.3%;
54.8%;
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#2116.
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cellular proliferation
 Score
Pred.
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polynucleotide
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Pred.
                                                 BP.
polynucleotide
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No. 1.
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No. 1.5e+02;
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1.3e+02;
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.5e+02;
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.3e+02;
 DB 5;
.6e+02;
                                                                                DB 5;
.6e+02;
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.6e+02;
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.4e+02;
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.3e+02;
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Query Match
Best Local Similarity
RESULT 1177
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Best Local Similarity
RESULT 1176
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Best Local Similarity
RESULT 1175
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Best Local Similarity
RESULT 1173
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RESULT 1171
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Best Local Similarity
RESULT 1170
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Human respiratory s
US2003215893-A1.
20-NOV-2003.
                                                                                                                                                                                        Human 30ST4 genc
W0200292849-A2
21-NOV-2002
                                                                                                                                                                                                                                                                       AAQ04668 standard; DNA; 12036 BP.
FHA structural gene, fhaB.
WO9004641-A.
03-MAY-1990.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(ISTS ) SCLAVO SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 3-OST-4 5' WO9922005-A2.
                                                                                                     FMR2 coding sequence.
                                           (INRM ) INSERM INST NAT SANTE 2.3%; STY Match 2.3%; ST Local Similarity 49.5%; I
                                                                                                                                                                                                               ABZ23912 standard, I
Human 3OST4 genomic
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RY Match
2.3%; Score 34.:
Local Similarity 53.7%; Pred. No.
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Human digestive
WO200155314-A2.
                      AAK89020 standard; DNA;
                                                                                           WO9967395-A1.
                                                                                                                                                               (ASTR ) ASTRAZENECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA10263 standard; DNA; 11883 BP.
Bordetella pertussis filamentous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human respiratory US2003077704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI97560 standard; DNA; 4172 BP.
Human respiratory system associated polypeptide-related DNA SeqID1024.
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                                                                                 29-DEC-1999
                                                                                                                 ABN97984 standard; DNA; 13695
                                                                                                                                                                                                                                                                                                                                                                                               (RELM/) RELMAN D A.
(DOME/) DOMENIGHINI
(RAPP/) RAPPUOLI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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th 2.3%;
Similarity 57.3%;
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system associated
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           antigen
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                      32152 BP.
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                                            Score 34.8; DB 3;
Pred. No. 3e+02;
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Pred.
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         genomic
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No. 2.
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No. 1.
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No. 2.
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No. 1.7e+02;
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No.
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No. 1.7e+02;
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           sequence
                                                                                                                                          DB 8;
.9e+02;
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.8e+02;
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.7e+02;
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.8e+02;
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.6e+02;
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02-AUG-2001

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Best Local Similarity
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RESULT 1183
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RESULT 1178
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                                                                                                                                                                                                     Human colorectal cancer related polypeptide DNA US2003054420-A1.
                                          WO9911799-AZ.
                                                              AAX23520 standard;
                                                                                                                           WO200157182-A2.
                                                                                                                                  AAK66362 standard; DNA; 3693
Human immune/haematopoietic
                                                                                                                                                                                    20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                             ADB32581 standard; DNA; 32152 BP.
Human novel colon related polypeptide DNA
US2003050231-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ABS99968 standard; DNA; 32152 BP.
Genomic DNA #172 encoding human colorectal cancer
US2002119919-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence WO200155302-A2.
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Human colorectal ca
WO200155350-A1.
                                11-MAR-1999
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                     (MEDI-)
                                                                                                      (HUMA-) HUMAN GENOME
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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MEDICAL COLLEGE GEORGIA RES INST.

1. 2.3%; Score 34.8;
Similarity 54.8%; Pred. No. 5.
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#40 encoding
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                                                  DNA; 45546
peptidase P
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55.9%;
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Pred. No. 5.5e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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Best Local Similarity
RESULT 1196
ID ACN44002 standard; D
DE Human genomic sequen
PN WO2003073826-A2.
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RESULT 1187
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Best Local Similarity
RESULT 1195
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Query Match
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                                                                                              ADL13775 standard; DNA; 173805 BP. Osteoarthritis-associated polymorphic WO2003054166-A2.
                                                                                                                                                                                          ABD33312 standard; DNA; 138115 BP. Murine cancer-associated (CA) gene W02004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse genomic sequence mCG21419. WO2003073826-A2.
           ACN44002 standard; DNA; 228139 E
Human genomic sequence hCG37533.
                                                                                                                                                                                                                                         (PROT-) PROTEIN DESIGN LABS INC.
ry Match 2.3%; Score
t Local Similarity 54.8%; Pred.
                                                                                                                                                                                                                                                                              WO2004048938-A2.
10-JUN-2004.
                                                                                                                                                                                                                                                                                                                 ADQ17592 standard; DNA; 116561 BP
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Mouse cancer associated sequence MD08-035, W02204060304-A2.
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ry Match 2.3%;
t Local Similarity 53.7%;
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tch 2.3%; Score
al Similarity 50.6%; Pred
                                              INCYTE GENOMICS INC.
h 2.3%;
Similarity 53.7%;
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Pred. No. 6
                                                                                                                                                                                                         gene
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No. 8.
                                                 34.8; DB 10;
No. 1.1e+03;
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No. 6.
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7
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5.9e+02;
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.4e+02;
                                                                                                                                                                                                                                           DB 12;
.7e+02;
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.5e+02;
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LETY MATCH
BEST LOCAL Similarity
RESULT 1205
ID ABS28139 Stand-
DE Human liv-
PN WO200
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METCH
METCH
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MESULT 1204

ID AAKO3087 star-
DE Human br-
PN WO20
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ID AAI3446
DE Probe #
PN WO20015
PD 09-AUG-
PA (MOLE-)
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RESULT 1201
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                                                                                            Human brain expressed single
                                                                                                                                                           Human bone marrow WO200157276-A2.
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                                                                                                     AAK03087 standard; DNA; 422
                                                                                                                                                                             AAK28539 standard;
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                                                                                                                                                                                                                                                   ABA24575 standard; DNA; 422
                                                                                                                                                                                                                                                                                                          Human breast cell single exon nucleic WO200157271-A2.
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Probe #3149 used to measure
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Human foetal liver single exon nucleic
WO200157277-A2.
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SSG #9.
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Similarity 64.2%; Pred.
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Similarity 48.1%;
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                    DNA; 422 BP. exon probe,
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RESULT 1208
                                      Best Local Similarity RESULT 1213
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RESULT 1211
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Pseudomonas aeruginosa polynucleotide #2298.
US6551795-B1.
22-APR-2003.
                                                                                      Human GPCR gene, WO2003000893-A2.
                                                                                                 Human GPCR
                                                                                                                                                                                                                                                                   Plant cDNA #3630.
US2004016025-A1.
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(UYMC-) UNIV MCGILL.
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WO2003000898-A1.
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                                                                                                          ADC12755 standard;
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                             ABD03694 standard; DNA; 984 BP
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KREPS J.
PROVART N.
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BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
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th 2.3%; Score
Similarity 47.1%; Pred.
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ZHU T.
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SEQ ID No 8
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RESULT 1217
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RESULT 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                     (FEDE/) FEDER J N. (MINT/) MINTIER G. (RAMA/) RAMANATHAN C (HAWK/) HAWKEN D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding human GPCR HF1948. WO200268600-A2.
                                                                                           Human G-protein 
US2004161823-A1.
                                                                                                                                                                                                                                                                                                    Human cDNA encoding US2003129653-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding novel US2003022186-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABT04869 standard; cDNA; 1086 BP. Human G protein coupled receptor hRUP31 coding W0200242461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR18583 standard; cDNA; 1083
Human GPCR 14273 coding sequer
WO2004065960-A1.
05-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2002.
(UYMC-) UNIV MCGILL.
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Mouse and human consensus SCE1 nucleotide sequence
WO200288352-A2.
                                                                                                                              ADR40535 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA60998 standard;
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ry Match 2.3%;
t Local Similarity 53.3%;
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ry Match 2.3%;
t Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                        ADB47641 standard; cDNA; 1086 BP.
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(MINT/) MINTIER G.
(RAMA/) RAMANATHAN
                                                          FEDE/)
                                                                            9-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AREN-) ARENA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
FEDER J N.
) MINTIER G.
) RAMANATHAN C.
) HAWKEN D R.
                                                                                                                                                                    Similarity
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                                                                                                             coupled
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GPCR HF1948
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2.3%;
53.3%;
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53.3%;
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                                                                                                             receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence,
                                                                                                                                1086
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No. 98
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No. 93;
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No. 98;
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No.
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No. 98;
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No. 93;
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98;
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                                                                                                               CDNA
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Query Match
Best Local S
RESULT 1229
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Best Local S
RESULT 1223
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Best Local Similarity
RESULT 1226
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RESULT 1225
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Best Local Similarity
RESULT 1224
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(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

2.3%; Score 34.6; DB 10;

ery Match

2.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                        AAI66039 standard; cDNA; 1458 BP. Human G protein-coupled receptor encoding JP2001211885-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human G-protein coupled receptor-20 WO200142288-A2.
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US2002151705-A1.
17-OCT-2002.
                                                                                                        ADR01275 standard; DNA; 1599 BP. Farnesyl dibenzodiazepinone biosynthetic
                                                                                                                                                                                                                                                                                                            ADC87380 standard; I
Human GPCR gene SEQ
DNA encoding a WO200050596-A2.
                       AAA64346 standard; DNA; 1743
                                                                                              WO2004065591-A1.
                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.

ry Match 2.3%;
t Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT44390 standard; cDNA; 1368 BP.
Bacterial polynucleotide #19141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
ry Match 2.3%;
t Local Similarity 53.3%;
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Bacterial polynucleotide
US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABX10627 standard;
                                                                    (ECOP-) ECOPIA BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                   (HINK/) HINKLE G
(SLAT/) SLATER S
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003233675-A1.
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SLATER S
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                                               Similarity
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Q ID NO:1833.
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orphan
            G-protein
                                               2.3%;
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                                               Score
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Pred.
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Pred. No. 1.1e+02;
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Pred.
           coupled
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No. 98;
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No. 1e+02;
                                               34.6;
No. 1.
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No. 1.1e+02;
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           receptor designated 14273
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.1e+02;
                                               DB 13;
.2e+02;
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.1e+02;
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Best Local Similarity RESULT 1236
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PA DE D
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                                                   RESULT 1238
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                                                                                                                                                Query
Best I
                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB53747 standard; DNA; Primary rat hepatocyte tWO2003065993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF70511 standard; DNA; 1800 BP. Orphan receptor ligand-related human WO2003071272-A1.
                                                                                                                                                                                         ADA70561 standard; DNA; Rice gene, SEQ ID 3884. WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ81226 standard; c
Human 14273 nucleic
                    EP1308459-A2.
                                                                                                      Prokaryotic essential gene WO200277183-A2.
                                                                                                                             ACA50840 standard;
                                                                                                                                                                                                                                                                                       ADO28989 standard; cDNA; 2081 BP.
Human novel GPCR PGR4 polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC.
2.3%;
ry Match 2.3%;
t Local Similarity 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003064624-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB58993 standard; DNA;
Toxicity-related gene, 9
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ry Match 2.3%;
t Local Similarity 53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2003
                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG

CY Match 2.3%; Score

: Local Similarity 49.2%; Pred.
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cy Match 2.3%;
Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC.
                                                                                  ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                          Match 2.3%; occal Similarity 51.6%;
                                                                                                                                                                                                                                                                                                                         ocal Similarity
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                                                                                                                                                                                                                                                        PRIMAL INC.
                              encoding
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                              cDNA; 2
g clone
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c acid, associated with metabolic
                                                                                                                            DNA;
                                                            I INC.
2.3%;
46.5%;
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toxicity modelling
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SEQ ID
                                                                                                               2355 BP.
ene #32497.
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                           2650 BP.
e TESTI20287760
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D 4019
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No. 1.
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No. 1.2e+02;
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.3e+02;
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.3e+02;
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.3e+02;
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.3e+02;
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.2e+02;
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RESULT 1242
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                                                       AAA10594 standard; DNA; 10732 BP. Gene encoding a subunit of cellulose JP2000060568-A.
                                                                                                                                              ADR01273 standard; DNA; 5960 BP. Farnesyl dibenzodiazepinone biosynthetic WO2004065591-A1.
                                                                                                                                                                                        (IBAR-) IBARAKI PREFECTURE.
xry Match 2.3%;
t Local Similarity 56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human soft tissue WO2004048938-A2.
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"ITY Match 2.3%;
It Local Similarity 56.6%;
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Pseudomonas aeruginosa polynucleotide
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Human soft tissue sarcoma-upregulated
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2-DEC-2002.
(KAZU-) KAZUSA DNA RES INST FOUND.
(PROT-) PROTEIN EXPRESS CO LTD.
2.3%; Score
55.4%; Pred.
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Human gene sequence #3.
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                                                                                                                         (ECOP-) ECOPIA BIOSCIENCES
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W0200299103-A1.
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                      /) MIZUNO K.) OJI PAPER
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DI FRANCESCO V.
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.5e+02;
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.3e+02;
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.8e+02;
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.8e+02;
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.7e+02;
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       Human DNA sequence WO200151659-A2.
                        AAH88704 standard;
                                                                            WO2004060304-A2.
                                                                                     ADQ97700 standard; DNA;
Mouse cancer associated
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                                                                                                                                                                                                                                                                          ABD33307 standard; DNA;
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CY Match 2.3%;
Local Similarity 54.3%;
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) WEBSTER M.
) KETCHUM K A.
) DI FRANCESCO V
) BEASLEY E M.
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th 2.3%;
Similarity 54.3%;
                                        SAGRES DISCOVERY INC. h 2.3%; Similarity 50.9%;
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               DNA; 160755 BP.
SEQ ID 544.
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genomic DNA MD12-027.
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No. 5e+02;
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.8e+02;
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Best Local Similarity RESULT 1264
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                                                                     Alternatively spliced form of WO200129235-A2.
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Human target of methylation-induced
WO20012925-A2.
26-APR-2001.
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Human colon cancer WO200055351-A1.
                   AAC98638 standard;
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                                                                                                                                                                    Novel DNA-related
                                                                                                                                                                                                                                      DNA encoding novel WO200175067-A2.
                                                                                                                                                                                                                                                        AAS75428 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN44110 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                            (UYEM-) UNIV EMORY.
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(PFIZ ) PFIZER PROD INC.
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                                                          (UYEM-) UNIV EMORY.
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Similarity 53.3%;
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human
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         antigen nucleotide sequence
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Pred.
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Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.4;
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence SeqID28
                                                                                                                     34.4;
No. 66;
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No. 66;
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No. 1.
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No. 1
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No. 1.
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                                                                                        TMS1
                                                                                                                                                                                                                                                                                                                            protein
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                                  *.4;
68;
                                                                                                                                                                                                                                                                                                                                                      4.4;
62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
.5e+03;
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.2e+03;
                                                                                       CDNA
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                                                                                                                              BB
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                                                4;
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          SEQ
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                                               Length
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           IJ
           NO:648
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                                                                                                                              379;
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HUMAN

GENOME

SCI INC.

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Best Local Similarity
RESULT 1273
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RESULT 1272
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                                                                                                                                                           RESULT 1271
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2 2 I
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                                 Query Match
Best Local
                                                                                                                                                               Best Local Similarity
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                                                                        ABS56032 standard; cDNA; 740 BP. cDNA encoding human caspase recr
                                                                                                                                                                                                                                                                                                                                                                                                       AAD03891 standard; DNA; 626
CpG island of human TMS1 ger
W0200129235-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana EP1033405-A2.
Human novel cytokine
WO200175093-Al.
              AAS59817 standard;
                                                                                                                                 Human caspase recruitment WO200244354-A2.
                                                                                                                                                  ABK87967 standard;
                                                                                                                                                                                                   Human caspase r
WO200244354-A2.
                                                                                                                                                                                                                    ABK87966 standard;
                                                                                                                                                                                                                                                                     WO200100826-A2.
                                                                                                                                                                                                                                                                              AAF30007 standard;
Human CARD-5 cDNA.
                                                                                                                                                                                                                                                                                                                                      Alternatively s
WO200129235-A2.
                                                                                                                                                                                                                                                                                                                                                      AAD03906 standard; cDNA;
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Arabidopsis thaliana DNA fra
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Bovine EST associated with lactation/muscle/fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002137139-A1.
                                                                                                                                                                                   (MILL-) MILLENIUM
                                                 (BERT/) BERTIN J.
                                                                                                                                                                                                                                                                                                                       UYEM-) UNIV EMORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN
(TAON/) TAO N.
                                                          2-SEP-2002
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2.3%;
ty 46.0%;
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2.3%;
46.0%;
              CDNA;
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      encoding
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fragment
              745
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domain-5
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       CDNA
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No. 70;
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No. 92;
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No. 71;
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                               34.4;
No. 92;
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No. 92;
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No. 92;
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No. 90;
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No. 84;
      790CIP2B_1
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Best Local
RESULT 1282
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Best Local Similarity
RESULT 1280
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                                                                                                                                                                                                                         Human cancer associated gene WO200055350-A1.
                                                                                                                                                    ADR01252 standard; DNA; 825 Farnesyl dibenzodiazepinone W02004065591-A1.
                                                                                                                                                                                                                                                                                                   Human colon cancer antigen WO200122920-A2. 05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                       ADF90785 standard; DNA; 796 BP. Human hepatic-fibrosis disease marker JP2003259877-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL47126 standard; DNA; 782 BP. Byrin domain containing protein WO200240668-A2.
23-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD03890 standard;
Human target of mei
Human TMS1 DN/
DE10255104-A1
                   ADP07316 standard;
                                                                          Antipsoriatic cD
WO2004028479-A2.
                                                                                                                                             05-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human breast to DE19813839-A1.
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                                                                                              ADN05025 standard;
                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
ry Match 2.3%;
t Local Similarity 46.0%;
                                                                                                                                                                                                                                                                                                                                  AAH34052 standard;
                                                                                                                                                                                                                                                                                                                                                                       (SUMU)
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                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                               ECOPIA BIOSCIENCES 1
h 2.3%;
Similarity 54.8%;
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                                    Similarity
                                                        GENENTECH
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tumour-associated 1
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                                                                                    CDNA
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                                                                                   cDNA; 936
sequence #
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2.3%; Score:
46.0%; Pred. 1
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2.3%; Score
46.0%; Pred.
                   DNA; 936
                                                                                                                                                                                                                                                                                                                       cDNA; 806 BP. antigen encoding
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                                     2.3%;
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                    ВP
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biosynthetic
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Pred.
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                                     34.4; DB
No. 1e+02;
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No. 96;
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No. 95;
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34.4;
No. 9
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No. 93;
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No. 92;
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No
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96;
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                                                                                                                                                              protein
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Best Local Similarity
RESULT 1287
ID AAS277...
                                                            Best Local Similarity RESULT 1290
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PA
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RESULT 1288
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Best Local Similarity
RESULT 1285
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Best Local Similarity
RESULT 1283
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RESULT 1284
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                                                                                                                                                                              02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
2.3%;
                      Human neoplastic disease-associated US2003082758-A1.
                                                                                                                                 Human cDNA encoding US2002168711-A1.
                                                                                                                                                                                                                WO200155163-A1.
                                                                                                                                                                                                                      AAS34830 standard; cDNA; 1619 BP. cDNA encoding novel human neoplastic
                                                                                                                                                                                                                                                                                             AAS27365 standard; cDNA; 1619 BP. cDNA encoding novel signal transduction WO200154733-A1.
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aer
WO200170955-A2.
27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                      AAS54218 standard; DNA; 1470 BP. Pseudomonas aeruginosa DNA for c
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADT46829 standard; cDNA;
Bacterial polynucleotide
US2003233675-A1.
                                                                                       (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                    ADB93543 standard;
                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
ry Match 2.3%;
t Local Similarity 46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neuroblastoma WO200166719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
ry Match 2.3%; Score
t Local Similarity 46.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004039956-A2.
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Human PRO cDNA sequence SEQ ID NO:2253.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI97783 standard; cDNA; 1049
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HUMAN GENOME SCI INC.
                                                                                                                                        cDNA; 1619
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP. polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                      cellular
34.4;
                                                                    34.4;
No. 1.
                                                                                                                                                                       34.4; DB
No. 1.4e+0
                                                                                                                                                                                                                                                      34.4;
No. 1.
                                                                                                                                                                                                                                                                                                                                    34.4; DB 4;
No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                    34.4;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.4; DB 4;
No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.4; DB
No. 1e+02;
                                                                                                                                          #390.
                                        gene
                                                                                                                                                                                                                       disease associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; DB 1
1e+02;
                                                                                                                                                                                                                                                                                                       pathway
                                                                    DB 10;
.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                     proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13;
..le+02;
                                                                                                                                                                       DB 4;
.4e+02;
                                                                                                                                                                                                                                                     DB 4;
.4e+02;
                                        64 cDNA
DB
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                       protein,
                                                                                                                                                                               Length 1619;
                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                              Length
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Length 1619;
                                                                             Length 1619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                     protein #349
                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                                                                                               1619
                                                                                                                                                                                                                                                                                                       Seq ID 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
RESULT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
RESULT
                                                                                                           Best Local
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
CDNA encoding no US2002132291-A1.
                                                                                                                                                                                                                                                                                                       (PENA,
                                                                                                                                                                                                                                                                                                                (MMIL)
                                                                                                                                                                                                                                                                                                                                   (ZHON/
                                                                                                                                                                                                                                                                                                                                                                                    (ZERH/
                                                                                                                                                                                                                                                                                                                                                                                                         (GORM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                        (KEKU/
                                                                                                                                                                                                                                                      CASM
                                                                                                                                                                                                                                                                                                                                                                            PADI
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Query Match
Best Local Similarity
RESULT 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1291
ID ADF30323 standard;
DE Human cancer suppre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1293
                                                                                                                                                                                              Best Local Similarity
RESULT 1295
                                                              AAS44718 standard; I
Human full-length po
WO200164834-A2.
07-SEP-2001.
                                                                                                                                                              Human target of WO200129235-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding novel signal WO200154733-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer suppressing protein PP10443-encoding CN1368508-A.
11-SEP-2002.
(SHANGHAI INST ONCOLOGY.
             ABX14762 standard;
                                                                                                                                                                                  AAD03889 standard; DNA; 2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                     (HYSE-) HYSEQ INC.
                                                                                                                                         (UYEM-) UNIV EMORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ50974 standard; cDNA; 2:
Human cDNA encoding NOV15a
US2004030096-A1.
12-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA encoding US2002168711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
2.3%;
It Local Similarity 50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB93191 standard;
                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                              PENA C E A.
BURGESS C E.
SCIORE P.
STONE D J.
TAUDIER R J.
CASMAN S J.
ROTHENBERG M E.
                                                                                                                                                                                                                           MALYANKAR U M.
BOLDOG F L.
                                                                                                                                                                                                                                                                                                                                             ZHONG M.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                               PADIGARU M. GUO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                     MILLER C E.
                                                                                                                                                                                                                                                                                                                                                                                                  ZERHUSEN B D.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                         GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                   KEKUDA R.
novel
                                                                                                                                                                        rd; DNA; 2821 BP.
methylation-induced
                                                                                  ; DNA; 3321 BP.
polynucleotide
            CDNA; 3380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA; 2686
  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a novel
                                 2.3%;
                                                                                                                    2.3%;
                                                                                                                                                                                                      2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2768 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2686 BP.
  ras-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                 Score
Pred.
                                                                                                                    Score
Pred.
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Pred.
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Pred.
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Pred.
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                                                                                    sequence
                                                                                                                                                                                                      34.4;
No. 1.
                                                                                                                    34.4;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.4;
No. 1.
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  protein.
                                 34.4; DB 4;
No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.4;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.4; DB 10;
No. 1.7e+02;
                                                                                                                                                                     silencing-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4e+02;
                                                                                                                                                                                                      DB 12;
..8e+02;
                                                                                                                    DB 4;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathway protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
.7e+02;
                                                                                     #143
                                                                                                                                                                        (TMS1)
                                          Length 3321;
                                                                                                                             Length 2821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA,
                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                      genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ:10 and
                                                                                                                                                                                                                  2768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq ID
                                                                                                                                                                         DNA.
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METTA IN NETHERLANDS

WHICH

WEST LOCAL SIMILARITY

RESULT 1304

ID ABN95047 stand

DE Gene #1547

PN WO200
                                                                                                                                                                                                  PAPREI
                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 130:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1299
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local
                                         AAL06946 standard; DNA; 12232 BP. Human reproductive system related W0200155320-A2.
                                                                                                                              ABN95047 standard; DNA; 4702 BP. Gene #1545 used to diagnose liver W0200229103-A2.
                                                                                                                                                                                                                              ADR24345 standard; DNA; 4670 BP.
Breast cancer prognosis marker #206.
WO2004065545-A2.
                                                                                                                                                                                                                                                                                                                    AAV15181 standard; cDNA to mRNA; 3955 Human serrate 2 encoding cDNA. W09802458-A1.
                                                                                  (GENE-) GENE LOGIC INC. 2.3%; cy Match 2.3%; Local Similarity 51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                           WO2003066831-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                     Angiogenesis-differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK65790 standard; DNA; 3438 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTSIG encoding WO2004001005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH61306 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
ry Match 2.3%;
t Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast cancer re
US2003099974-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cancer WO200151628-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL26787 standard;
                                                                                                                                                                                                                                                                                                                                                                (ORIG-) ORIGENE TECHNOLOGIES cy Match 2.3%; Local Similarity 50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE ry Match 2.3%; st Local Similarity 52.9%; I
                                                                                                                                                                                                (ROSE-) ROSETTA INPHARMATICS LLC.
                                                                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KOGYO KK.

CY Match

2.3%;
Local Similarity

51.3%;
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) KETCHUM K A.
) DI FRANCESCO
) BEASLEY E M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCYTE CORP.
                     HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 3420 BP.
A 7512389CB1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA; 3399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed
                                                                                                                                                                          2.3%;
2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    expressed
                                                                                                                                                                                                                                                                                                                                                                INC.
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E MEDICINE INC.
Score 34.4; DB :
Pred. No. 2e+02;
Score
Pred.
                                                                                    Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                          cancer.
                                                                                                                                                                                                                                                                                                                                                              34.4; DB 1
. No. 2e+02;
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                                                     antigen
34.4;
No. 3.
                                                                                                                                                                                                                                                                           34.4;
No. 2.
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No. 2e+02;
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No. 2e+02;
                                                                                                                                                                          34.4; DB 13;
No. 2.3e+02;
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No. 2e+02;
                                                                                     34.
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                   DB 6;
.3e+02;
DB 4;
.7e+02;
                                                                                                                                                                                                                                                                           DB 2;
.le+02;
                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                     SEQ
                                                                                                                                                                                                                                                                                    Length 3955;
         Length 12232;
                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                     NO:
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Best Local Similarity RESULT 1313
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        Query Match
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WO9724435-A1.
10-JUL-1997.
(DARW-) DARWIN MOLE
                                                                                           O2-JAN-2003.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

2.3%; Score 34.4; DB 10;

ery Match

2.3%; Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2004.
15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
2.3%;
27 Match 2.4milarity 44.2%;
                                                      Corn seedling-derived US2003237110-A9.
                                                                                                                                                                                                                     (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
ry Match
t Local Similarity 53.8%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR01210 standard; DNA; 36602 BP. Farnesyl dibenzodiazepinone biosynthetic WO2004065591-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine cancer-associated WO2004058146-A2.
                                                                               ADS67678 standard;
                                                                                                                                                                       Human GPCR gene
EP1270724-A2.
                                                                                                                                                                                  ADC86916 standard; DNA; 349989 BP.
Human GPCR gene SEQ ID NO:1369.
                                                                                                                                                                                                                                                                                                     AAH41223 standard; DNA; 349980 BP.
Pyrococcus abyssi genomic fragment
                                                                                                                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.3%;
t Local Similarity 54.8%;
                                                                                                                                                                                                                                                                                                                                                                                              WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          ADQ97651 standard; DNA; 127943 BF
Human cancer associated sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genomic se
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse genomic se
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN45024 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABD33201 standard; DNA; 36312 Murine cancer-associated (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX83006 standard; DNA; 16442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACN44818 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAGR-) SAGRES DISCOVERY.

ry Match
Local Similarity 55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
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2.3%; Score

47.6%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOPIA BIOSCIENCES INC.
h 2.3%; Score
Similarity 54.8%; Pred.
                            INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence hCG30155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic sequence
                                                                  cDNA; 238 BP.
red polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.3%;
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                                                                                                                                                                                                                                                                                                      fragment
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Pred.
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Pred.
    Score
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Pred.
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nce HD10-021,
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No. 1.
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No. 4.
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No. 1.
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No. 1.
    NO.
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No.
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No. 6.
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No. 6.
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1.2;
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                                                                  (cpds),
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4.3e+02;
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1.1e+03;
                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                           DB 12;
.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
.7e+02;
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.4e+02;
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.4e+02;
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RESULT 1315

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BESULT 1323
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RESULT
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RESULT 1321
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Best Local Similarity
RESULT 1319
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Best Local Similarity
RESULT 1318
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Best Local Similarity
RESULT 1317
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                                 Rice gene, SEQ I
WO2003000898-A1.
                                        ADA69917 standard; DNA; 978 Rice gene, SEQ ID 3240.
                                                                                                                                                                         AAS69547 standard;
DNA encoding novel
WO200175067-A2.
                                                                                                     DNA encoding novel WO200175067-A2.
                                                                                                                       AAS75461 standard;
                                                                                                                                                                                                                                               Human ovarian c. WO200192581-A2.
                                                                                                                                                                                                                                                                                                                  Nucleotide sequence WO200153524-A2.
                                                                                                                                                                                                                                                                                                                                                                                              AAF07736 standard;
Fusarium venenatum
WO200056762-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast
                                                                                                                                                                                                                                                              ABL87669 standard; cDNA; 695
                                                                                                                                                                                                                                                                                    26-JUL-2001.
(UYNO-) UNIV NOTTINGHAM TRENT.
2.3%; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200264611-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker WO200160860-A2.
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(FINC/) FINCHER K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cotton expressed US2004123338-A1.
                                                                                                                                                                                                                                                                                                                                  AAH42837 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP94454 standard; cDNA; Cotton expressed sequence
                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO NORDISK BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABT07648 standard;
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                SYNGENTA PARTICIPATIONS AG
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                                                                                                             cDNA;
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2.3%; S
55.5%; P
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e of a human m
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EST SEQ ID NO
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2.3%;
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                                                                                                                                                                                 708 BP.
diagnostic
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diagnostic
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e tag,
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EST,
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                                                                  No. 1e+02;
34.2;
No. 1.
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No. 1e+
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No. 77;
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No.
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No. 97;
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No.
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No. 65;
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79;
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DB 8;
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+02;
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RESULT 1324
ID AAQ6721
DE Human c
PN CA21116
                                   Best Loca
RESULT 1332
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RESULT
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Best Local Similarity
RESULT 1330
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RESULT 1329
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RESULT 1327
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AAX86357 standard;
Rat smooth muscle n
WO9936101-A1.
                                                                                                   AAK69400 standard; DNA; 11456 Bp.
Human immune/haematopoietic antigen
                                                                                                                                                                                 Sorangium cellulosum tmbA
US2003054547-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker r. WO200142467-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial polynucleotide US2003233675-A1.
                                                                                                                                                                                             ADC26983 standard; DNA; 11358 BP.
Sorangium cellulosum tmbA gene cluster tmbC DNA
                                                                                                                                                                                                                             (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

TY Match
2.3%; Score 34.2; DB 13;

TOTAL Similarity 56.8%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                           Human sidekick homologue WO2004076622-A2.
                                                                                                                                                                                                                                                                                                                                                                   PRO polypeptide WO2004041170-A2.
                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
2.3%; Score 34.2; DB 4;
t Local Similarity 53.3%; Pred. No. 2.2e+02;
                                                                                          WO200157182-A2.
                                                                                                                                                                                                                                                                                                   ADR83544 standard;
                                                                                                                                                                                                                                                                                                                                                                             ADP25090 standard; cDNA; 3674 PRO polypeptide encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ67210 standard; DNA; 1423 Human corticosteroid binding CA2111656-A.
                                                                   (HUMA-) HUMAN GENOME
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ry Match 2.3%; Score 
t Local Similarity 47.6%; Pred.
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SLAT/) SLATER S
                                             Local Similarity
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                                                                                                                                                           JULIEN B.
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           myosin heavy
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                        DNA; 16009
                                                                                                                                                                                                                                                                                                                      2.3%;
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2.3%;
54.3%;
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#23431.
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DNA,
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globulin
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No. 4.
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e 34.2; DB 2;
. No. 1.4e+02;
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No.
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No. 1.
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No. 1
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           gene
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                                              . 2;
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.1e+02;
                                                                                                                                                                                                                                                                                                                      DB 13;
.3e+02;
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.8e+02;
                                             DB
1e+
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.6e+02;
                                            4;
+02;
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                                                                                                     ID NO:24212.
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Best Local Similarity
RESULT 1339
ID AAF88314 standard; Di
DE S. spinosa DNA fragme
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB ) BAYER AG.
                                                        Best Local Similarity
RESULT 1340
ID AAF88317 standard, D
DE S. spinosa DNA fragm
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB ) BAYER AG.
                             RESULT
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RESULT 1338
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                                                                            AAF88317 standard; DNA; 29736 BP. S. spinosa DNA fragment SEQ ID 6. DE19957268-A1.
                                                                                                                                                         AAF88314 standard; DNA; 25360 BP.
S. spinosa DNA fragment SEQ ID 3.
DE19957268-A1.
                                                                                                                                                                                                                                                                                                               Cephalosporin antibiotic
JP02291274-A.
03-DEC-1000
AAD56078 standard; DNA;
Mouse Map3k6 carcinoma a
WO2003035837-A2.
                                                                                                                                                                                                                                         ACN44414 standard; DNA; 24492 BP. Human genomic sequence hCG1780827 WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Sorangium cellulosum US2003054547-A1.
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(OWEN/) OWENS G K.
(MANA/) MANABE I.
                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                         ADC26981 standard; DNA; 20922 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human periodontal
WO2004042054-A1.
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23-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA60861 standard;
Rat smooth muscle r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200259270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN84504 standard; DNA; 16011 BP.
Rat smooth muscle myosin heavy chain gene (-4216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN37218 standard; DNA; 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VIRGINIA PATENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUBI-) HUBIT GENOMIX INC. (KAMO/) KAMOI K.
                                                                                                                                                                                                                                                                                                                                                                                 JULI/) JULIEN B.
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                            Local Similarity
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h 2.3%;
Similarity 60.0%;
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h 2.3%;
Similarity 45.6%;
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                                     2.3%;
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associated
                  32069
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Pred.
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                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
         (CA)
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No. 4.
                                     34.
No.
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No. 4.
                                                                                                                   34.
No.
                                                                                                                                                                                                 34.2; DB 11;
No. 5.9e+02;
                                                                                                                                                                                                                                                                               34.
No.
                                                                                                                                                                                                                                                                                                                                                              34.2; DB 10;
No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                            34.2;
No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.
No.
                                     1.2;
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                                                                                                                  .2; DB
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?
                                                                                                                                                                                                                                                                                                                                genes
        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α
                                                                                                                                                                                                                                                                                                                                                                                                               tmbB DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTGDS
                                     DB 4;
.5e+02;
                                                                                                                                                                                                                                                                                DB 2;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
.8e+02;
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.8e+02;
                                                                                                                                                                                                                                                                                          B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              +11795)
                                               29736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16011;
                                                                                                                                                                                                                                                                                                                                                                        20922;
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Best Local Similarity RESULT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1345
                                                                                                                                           Best Local Similarity
RESULT 1349
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 1348
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
RESULT 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1342
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MOUBE MB3346 CARCLING

WO2003057146-A2.

) 17-JUL-2003.

A (SAGR-) SAGRES DISCOVERY.

2.3%; SAGRES DISCOVERY.
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                   ACN45116 standard; DNA; 42772 BP. Mouse genomic sequence mCG8527. W02003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                            ADQ97084 standard; DNA; 38690 BP. Human cancer associated sequence W02004060304-A2.
ABS65032 standard; DNA; Invertebrate foraging be WO200259370-A2.
                                                                                                                                                     (SAGR-) SAGRES DISCOVERY.

"XY Match 2.3%;

It Local Similarity 48.7%;
                                                                                                                                                                                                                                                                                      ADA37416 standard; DNA; 41907
Human rDNA repeat unit.
US2003108914-A1.
12-JUN-2003.
                                                                                                        Human ribosomal DNA
US2002160970-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS12439 standard; DNA; 37590 BP. DNA encoding 1-aminocyclopropane WO200168879-A2.
                                                                    (HADL/) HADLACZKY G. (SZAL/) SZALAY A A.
                                                                                                                               ADA14747 standard;
                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.3%;
t Local Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS17367 standard; DNA; 33529
DNA sequence of S. cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAGR-) SAGRES DISCOVERY.
ry Match 2.3%;
t Local Similarity 46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Map3k6 gen
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2003
                                                                                                                                                                                          L2-SEP-2003
                                                                                                                                                                                                                                                                           (HADL/) HADLACZKY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KOSA-) KOSAN BIOSCIENCE.
ry Match 2.3%;
t Local Similarity 56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB72179 standard; DNA; 32069
                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGRES DISCOVERY.
h 2.3%;
Similarity 46.4%;
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                                                                                                                   DNA; 42998
A complete 1
                                                                                                                                                                                                                                                   2.3%;
                                             2.3%;
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           A; 42999 BP.
behaviour a
                                               Score
Pred.
                                                                                                                  8 BP.
repeating
                                                                                                                                                                                                                                                   Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
                                                                                                                                                      Score 34.2; DB 11;
Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
           associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carboxylate
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                                               34.2;
No. 7.
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No. 7.
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No.
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No.
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No. 6.
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No. 6.
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No. 6.
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No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2;
                                                                                                                                                                                                                                                      . 2;
                                                                                                                    unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                DB 12;
.5e+02;
                                               DB 8;
9e+02;
                                                                                                                                                                                                                                                   DB 9;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase
            human
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           DNA sequence
                                                         Length
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 37590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32069;
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                                                                                                                                                                Length 42772;
                                                                                                                                                                                                                                                                                                                                                           Length 38690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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ID DE PA PA PA PA
                                                                                       Best Local Similarity
RESULT 1358
                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1352
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                 02-SEP-2004.
02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
2.3%;
ery Match
2.3%;
                                                                ADA03083 standard; DNA; 93483 Mouse mCG17918 carcinoma assoc
                                                                                                                                                                  Genomic DNA encoding US2002132291-A1.
                                                     WO2003057146-A2.
                                                                                                                                                                                                 ABX14763 standard; DNA; 88191 BP
                                                                                                                                                                                                                                                                   Mouse cancer-associated WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                       ADC26995 standard; DNA; 67251 BP. Sorangium cellulosum tmbA gene cluster. US2003054547-A1.
                                                                                                                    (KETC/) KETCHUM K A.
(DFRA/) DI FRANCESCO
(BEAS/) BEASLEY E M.
                                                                                                                                                                                                                                                                                       ABD32576 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP84151 standard;
Human CA125 genomic
WO2004045553-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ribosomal DNA complete repeating US2004163147-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUN-2004.
(UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ97534 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-2002
                                                                                                                                                                                                                                                                                                                                   JULI/) JULIEN B.
                                                                                                                                                                                                                                                                                                                                               20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY INC.
cy Match
Local Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR43949 standard; DNA; 42999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HADL/) HADLACZKY G. (SZAL/) SZALAY A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003101480-A1.
29-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD61411 standard; DNA; 42999 BP.
Human ribosomal DNA (rDNA) repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NEUR-) NEUROSCIENCES RES FOR MATCH 2.3%; t Local Similarity 47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HADL/) HADLACZKY G.
Local Similarity
                                                                                                                                                                                                                                                                                                             Local Similarity
                       Match
                                                                                                                                                                                                                                                                                                                           Match
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                                SAGRES
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        3 DISCOVERY.
2.3%;
arity 53.3%;
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                                                                                               2.3%;
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                                                                                                                                                                                       novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%;
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amino
                                                                                                                                                                                                                                                                           80423 BP.
genomic DNA MD7-205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        58687 BP.
sequence MD09-010,
                                                                associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S FOUND INC.
3%; Score 34.2;
4%; Pred. No. 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat region.
          Score 34.2; DB 9;
Pred. No. 1.1e+03;
                                                                                               Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                                              34.
No.
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No. 1.
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No. 9.
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No. 9.
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No. 9.
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No. 7
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No. 7
                                                               gene,
                                                                                              . 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unit.
                                                                                                                                                                                                                      DB 13;
.1e+03;
                                                                                                                                                                                                                                                                                                           DB 10;
.8e+02;
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.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
).1e+02;
                                                                                               DB 8;
.1e+03;
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.9e+02;
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.9e+02;
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.9e+02;
                                                               SEQ
                                                                                                                                                                                      protein
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                  Length
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                                                               NO:1601
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 58687;
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                  93483;
                                                                                                          88191;
                                                                                                                                                                                                                                80423;
                                                                                                                                                                                                                                                                                                                      67251;
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RESULT 1368
ID ADP7518
DE Human E
PN WO20030
PD 17-APR-
PA (GENO-)
                                                                                                                                           Query Match
Best Local Similarity
RESULT 1367
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Best Local Similarity
RESULT 1365
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1363
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                                                               Best Local Similarity
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                       Mouse cancer-associated WO2004074320-A2.
                                                                                                           ADF51132 standard; DNA; 243428 BP. Human P-Rex1 genomic DNA sequence. W02003080664-A1.
                                                                                                                                                                                                                                                                           ADL13512 standard; DNA; 178870 BP. Osteoarthritis-associated polymorphic nucleotide WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                            ABN95044 standard;
Gene #1542 used to
WO200229103-A2.
                      ADP75180 standard;
Human Endophilin 2
WO2003031594-A2.
                                                                                                                                                     (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.3%;
t Local Similarity 55.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2003.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E
                                                                                     (BABR-) BABRAHAM INST.
                                                                                                                                                                                                                                                    )3-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
2.3%;
                                                                                                                                                                                                                                                                                                                                                                  11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse genomic se
US2003216558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB72821 standard; DNA; 93483 Mouse mCG17918 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY.

"YY Match 2.3%;

It Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA66367 standard; DNA; 93483
Mouse mcG17918 gene genomic DN
WO2003053224-A2.
                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABD33157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL27161 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGRES DISCOVERY.

th 2.3%;
Similarity 53.3%;
  GENOME
 THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence for
                                gene;
                                                                                                                                                                                                                                                                                                                                INC.
2.3%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                     DNA; 110096 BP. diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 109559
ciated (CA) g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%;
                                                               2.3%;
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                                                                                                                                                                                                                                            50.9%;
                                                                                                                                                                                                          ; 227448 E
I genomic
                                            304905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93483 BP.
for mCG17918.
 CORP
                                                               Score
Pred.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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No. 1.
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No. 1.
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No. 1.
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No. 1.
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No. 1.
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No. 1.
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No. 1.1e+03;
                                                                                                                                                                                                            MD17-014
                                                                                                                                                     DB 13;
..7e+03;
                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
..le+03;
                                                                                                                                                                                                                                                                                                                                 DB 6;
.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
.2e+03;
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.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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                                                                          Length
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                                                                                                                                                                                                                                                    Length 178870;
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                                                                                                                                                                                                                                                                                                                                           110096;
                                                                           243428;
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16-OCT-2003

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Best Local Similarity RESULT 1375
                                                                                                                                                                                                                                                                                                                   RESULT 1372
                          Best Local Similarity RESULT 1376
                                                                                                                                                                                                                                                                                                                                                                BESULT 1369
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                                                                                                                                                                                                                                             RESULT 1373
                                                                                                                 Query Match
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                                                                                                                                                                                                          Human polynucleotide SEQ ID NO 4: WO200164835-A2.
ACH73361 standard; DNA; 510 Human genome derived single US2003194704-A1.
                                                                    cDNA sequence #607
WC200177289-A2.
                                                                                      ABK36216 standard;
                                                                                                                                                   Pseudomonas aeruginosa polynucleotide
                                                                                                                                                             ABD16714 standard; DNA; 429 BP
                                                                                                                                                                                                                                                                                                  DNA encoding novel
                                                                                                                                                                                                                                                                                                            AAS69541 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                    (LANG/) LANGE B M.
(GHAS/) GHASSEMIAN M.
(BRIG/) BRIGGS S P.
(COOP/) COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice isoprenoid
US2004010815-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG99503 standard; DNA; 280 BP.
Kidney disease-associated gene-related mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NITA-) JAPAN TAFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP07184657-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ98244 standard;
Exon 4 of rice pyro
                                                                                                                                           JS6551795-B1.
                                                                                                                                                                                                                                                                                         WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI45208 standard; cDNA; 378 BP
                                                              B-OCT-2001
                                                                                                                                                                                                HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                       HYSE-) HYSEQ INC
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Y Match 2.3%; Score 3
Local Similarity 47.2%; Pred. N
                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                Match
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                                GENETICS INST INC.
h 2.3%;
Similarity 52.0%;
                                                                                                       GENOME THERAPEUTICS h 2.3%; Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                               ZHU T.
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PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                   GOFF S A.
                                                                                                                                                                                                                                                                                                                                                                                  KREPS J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis-associated
                                                                                                                                                                                                                                                                                                  cDNA;
                                                                              encoding novel human
                                                                                       cDNA; 455 BP
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diagnostic
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Pred.
        BP.
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No.
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No.
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No. 2e+03;
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No.
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No.
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No.
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                                                                                                      DB
90;
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86;
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67;
         #6556
                                   DB
93;
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87;
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                                          Length
                                                                                                                                                                                       Length 400;
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                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence SeqID633.
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                                                                                                                  429;
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Query Match
Best Local S
RESULT 1383
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RESULT 1384
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RESULT 1382
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RESULT 1380
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RESULT 1379
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RESULT 1378
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Best Local Similarity
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(RANK/)
(HANZ/)
                                                             Human polynucleotide WO200157190-A2.
                                                                                                                                               Pseudomonas aeruginosa
US6551795-B1.
                                                                                                                                                                                                                                   ABD16865 standard; DNA; 1383 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
ABX05202 standard; cDNA; 2154 BP.
                                                                                    AAK52313 standard;
                                                                                                                                                                      ABD16805 standard; DNA; 1503 BP.
                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS ry Match 2.3%; t Local Similarity 49.4%;
                                                                                                                                                                                                                                                                                                              WO200175067-A2.
11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                   DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV06518 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa polynucleotide US6551795-B1.
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Rat gene AA799755,
WO2003016475-A2.
                                                                                                                                                                                                                           22-APR-2003
                                                                                                                                                                                                                                                                                                                                              AAS90702 standard;
                                                                                                                                                                                                                                                                                                                                                                                                              WO2004070035-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                       ADR46465 standard; DNA; 895 BP.
Tobacco caltractin-like protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS ry Match 2.3%; t Local Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABD16760 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPIT
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003.
(GEHO) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILL-) MILLENNIUM
                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                       ocal Similarity
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) RANK D R.
) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                          0035 ---- 2004
2004 ---- CO KGAA.
SUNGENE GMBH & CO KGAA.
2.3%; SCOTE 34;
46 9%; Pred. No.
                                                                                                    GENOME THERAPEUTICS h 2.3%; Similarity 49.4%;
                    Similarity
                                        HYSEQ INC.
                                                                       cDNA; 1627 BP.
de SEQ ID NO 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 521
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                   cDNA; 1167 BP. human diagnostic
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2.3%; Score 34;
46.6%; Pred. No.
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                   2.3%;
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                                                                                                                                                          polynucleotide
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No.
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                                                                                                       DB 11;
1.7e+02;
                                                                                                                                                                                           DB 11;
1.6e+02;
                                                                                                                                                                                                                                                #15469
                                                                                                                                                                                                                                                                               DB 5;
1.5e+02;
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1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                   DB 13;
1.3e+02;
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1e+02;
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#217

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Query Match
Best Local Similarity
RESULT 1393
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Best Local Similarity
RESULT 1391
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RESULT 1390
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Best Local Similarity
RESULT 1388
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RESULT 1387
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                                       AAL04774 standard;
                                                                                                      WO2004061080-A2.
                                                                                                              Rice stress-related
                                                                                                                          ADQ15650 standard;
                                                                                                                                                                            ADQ36980 standard; DNA; 2844 BP. Cell proliferation-related nucleic WO2004061122-A2.
                                                                                                                                                                                                                                                                   AAT35233 standard; cDNA; 2823 BP.
Matural killer lytic associated protein cDNA
WO9626744-A1.
                                                         (SYGN) SYNGENTA PARTICIPATIONS AG.

TY Match

Local Similarity

61.1%; Pred.
                                                                                                                                                                                                                                                                                                                                                  Human CDNA of the invention SEQ ID EP1347046-A1.
                                                                                                                                         (SYGN) SYNGENTA PARTICIPATIONS AG

xy Match 2.3%; Score

t Local Similarity 61.1%; Pred.
                                                                                                                                                                                                                                                (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                               06-SEP-1996
                                                                                                                                                                                                                                                                                                                                               24-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
2.3%; Score
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human coding sequence, SEQ ID 1067. EP1293569-A2. 19-MAR-2003.
                                                                                                                                                                                                                                                                                                                                 (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ87554 standard; cDNA;
Human tumour-associated a
WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour-associated a. WC2004060270-A2. 22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human novel polynucleotide WO200274961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                Local Similarity
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                         DNA; 3051 BP.
system related antigen DNA
                                                                                                            DNA; 2844
d protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC.
                                                                                                                                                                                                                             2.3%;
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SCI
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| antigenic
                                                                                                           coding
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Pred.
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Pred.
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Pred. No.
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No.
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No.
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No.
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No.
                                                          DB 12;
2.3e+02;
                                                                                                                                          DB 12;
2.3e+02;
                                                                                                                                                                                                                            DB 2;
2.3e+02;
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2.1e+02;
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2.1e+02;
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2e+02;
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2e+02;
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2e+02;
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                                                                                                            #30
                           SEQ
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PAPRI

ACC48895 standard; DNA; 12342

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Best Local Similarity RESULT 1402 ID ACC48895 standard;
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Best Local Similarity
RESULT 1401
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RESULT 1400
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Best Local Similarity
RESULT 1398
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RESULT 1396
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Best Local Similarity
RESULT 1394
                                 Query Match
                                                                                              02-JAN-2003.
(INSP ) INST PASTEUR.
(INSF ) INST FRANCAIS DU PETROLE.
(INSF ) ET FRANCAIS DU PETROLE.
2.3%; SCOTE
2.3%; Pred.
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                                                           ABL15220 standard; cDNA; 10479 BP. Drosophila melanogaster expressed W0200171042-A2.
                                        27-SEP-2001.
(PEKE ) PE CORP NY
                                                                                                                                                                ACC48896 standard; DNA; 870 Rhodococcus ruber eth gene EP1270722-A1.
                                                                                                                                                                                                         (NITA-) JAPAN TAFU GURASU KK.
iry Match 2.3%;
it Local Similarity 61.1%;
                                                                                                                                                                                                                                              AAQ98237 standard; DNA; 8626 BP. Partial rice pyruvate orthophosphate UP07184657-A.
25-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC64448 standard; DNA; 3896 BP. Arabidopsis thaliana PDAT genomic W020060095-A2.
                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                     23-AUG-2001
                                                                                                                                                                                                                                                                                                                                              Human proton/oligonucleotide transporter hPHT2 gene intron W0200160854-A1.
                                                                                                                                                                                                                                                                                                                                                                    AAH26524 standard; cDNA; 4182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC64438 standard; DNA; 3896 Bp. Arabidopsis thaliana PDAT genomic
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12-OCT-2000.
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Human prostate specific gene ;
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30-MAY-2002.
(DIAD-) DIADEXUS INC.
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th 2.3%;
Similarity 52.9%;
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2.3%;
52.9%;
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Jene cluster
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#3261.
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Pred. No.
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Pred. No.
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                                                                       polynucleotide
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                 DB 4;
4.4e+02;
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4.1e+02;
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2.8e+02;
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4e+02;
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2.7e+02;
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2.7e+02;
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2.7e+02;
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2.7e+02;
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2.4e+02;
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Query Match
Best Local Similarity
RESULT 1407
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                                                                                                                            Mouse pre rRNA gene.
US2004163147-A1.
                                                                                                                                                                                                                ACC44629 standard; DNA; 22118 BP. Mouse ribosomal RNA gene (rDNA) nucleotide WO200297059-A2.
                                                                                                                                                                                                                                                                                                   ADF10518 standard; DNA; 22118 Mouse ribosomal RNA gene repeaw02003093469-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          ĀADē1410 standard; DNA; 22118 BP.
Mouse ribosomal DNA (rDNA) repeat region.
            (INSP )
                                                   ACC48894 standard; DNA; 23656 BP. Rhodococcus ruber eth gene region
                                                                                                                                                 ADR43948 standard; DNA; 22118
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(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

ry Match
2.3%; Score 34;
ry Match
56.0%; Pred. No.
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US2003108914-A1.
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US2002160970-A1.
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WO200259265-A2.
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(SZAL/) SZALAY A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-OCT-2002.
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ry Match 2.3%;
Local Similarity 63.4%;
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            FRANCAIS
                     PASTEUR.
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DU PETROLE.
2.3%; Scor
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repeat unit.
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sequence
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6.4e+02;
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6.4e+02;
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6.4e+02;
                                                                                  DB 13;
6.4e+02;
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6.4e+02;
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6.4e+02;
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6e+02;
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Length 23656;
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Query Match
Best Local S
RESULT 1414
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Best Local S
RESULT 1412
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Best Local Similarity
RESULT 1419
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RESULT 1417
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RESULT 1415
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Best Local Similarity
RESULT 1413
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(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
Human immune/haematopoietic antigono200157182-A2.
                                                (HUMA-) HUMAN GENOME SCI INC.
Pry Match 2.3%;
St Local Similarity 57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic DNA #37 encoding US2002119919-A1. 29-AUG-2002.
                                                                                           Human colorectal US2003054420-A1.
                                                                                                                                                                                                       ABS99834 standard; DNA; 25424 BP. Genomic DNA #38 encoding human co US2002119919-A1.
                                                                                                                                                                                                                                                                                   AA157657 standard; DNA; 25424 BP. Human colorectal cancer antigen c WO200155350-A1.
02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                    AAK90280 standard; DNA; 25424 BP. Human digestive system antigen ge W0200155314-A2.
                                                                                                      ADB92987 standard; DNA; 25424 BP.
Human colorectal cancer related polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colorectal US2003054420-A1. 20-MAR-2003.
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Human colorectal cancer related polypeptide DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human digestive system antigen genomic WO200155314-A2.
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                                                                                   20-MAR-2003
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) RUBEN S M.
) BARASH S C.
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57.5%;
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RESULT 1422
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RESULT 1420
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       Mouse Gnb1 gene
WO2003008583-A2
                                          (SAGR-) SAGRES DISCOVERY.
ry Match 2.3%;
t Local Similarity 54.9%;
                                                                                              Human GNB1 gene.
                                                                                                      ADB72470 standard; DNA; 50396
                                                                                                                                                                  ADA02732 standard;
Human GNB1 carcinor
WO2003057146-A2.
                         ADB72467 standard;
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Human liver glucokinase genomic DNA.
WOZ00224741-A2.
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ry Match 2.3%;
t Local Similarity 54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      ACN44568 standard; DNA; 43799 Bp
Mouse genomic sequence mCG21498.
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WO200155449-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL56704 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ACN44568 standard;
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(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUM
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9.7e+02;
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                      ADE95749 standard; DNA; 96597 Mouse Bach2 gene genomic DNA & WO2003039484-A2.
                                                                                                       Mouse Bach2 gene. WO2003008583-A2.
                                                                                                                        ADB72239 standard; DNA; 96597
                                                                                              30-JAN-2003
                                                                                                                                          (SAGR-) SAGRES DISCOVERY.
ry Match 2.3%;
t Local Similarity 50.0%;
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                                                                                                                                                                                       WO2003057146-A2.
                                                                                                                                                                                                   Mouse Bach2
                                                                                                                                                                                                         ADA02501 standard;
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15-MAY-2003.
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RESULT 1446
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                                           ADL13501 standard; DNA; 167932 BP. Osteoarthritis-associated polymorphic
                                                                                                           ADQ59449 standard; DNA; Human cancer-associated WO2004058288-A1.
                                                                                                                                                                                                                                                    Human adenosine Al receptor antisense WC9913886-Al.
                                                                                                                                                                                 ABZ35015 standard; cDNA; 136328 BP. Human gene expression profile polynucleotide WO200274979-A2.
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ry Match 2.3%;
t Local Similarity 34.7%;
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(INCY-) INCYTE GENOMICS INC.
ry Match 2.3%;
t Local Similarity 57.5%;
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ry Match 2.3%;
Local Similarity 47.2%;
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1.4e+03;
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RESULT 1459
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Human bone marrow WO200157276-A2. 09-AUG-2001.
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Human foetal liver single
WO200157277-A2.
09-AUG-2001.
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                                                                     09-AUG-2001.
(MOLE-) MOLECULAR DYNAMICS
                                                                                              Probe #7553 used to WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding
                                 AAK33067 standard; DNA; 454
                                                                                                                     AAI38867 standard;
                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS
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Bovine EST associated with lactation/muscle/fat
US2002137139-A1.
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ry Match 2.3%;
t Local Similarity 54.4%;
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18-OCT-2001.
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29-MAY-2003.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS 2.3%; t'Local Similarity 49.7%;
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ry Match 2.3%;
t Local Similarity 48.7%;
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(MATH/) MATHIALAGAN
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No. 1e+02;
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5. 1.1e+02;
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1.1e+02;
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Best Local Similarity RESULT 1462
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RESULT 1468
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(MOLE-) MOLECULAR DYNAMICS INC.
(MOLE-) MOLECULAR DYNAMICS INC.
2.3%; Score
50.3%; Pred.
                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 8685.
WO200164835-A2.
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Human genome-derived single exon probe
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                                                                                                                                         Human ovarian cancer WO200170979-A2.
                                                                                                                                                                                                                                      ADD16019 standard; cDNA; 517 cDNA (SeqID 87) that confers WC2003020741-A1.
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                                                  Human cDNA clone EP1074617-A2.
                                                                                         27-SEP-2001.
27-SEP-2001.
(MILL-) MILLENNIUM PREDICTIVE
(xy Match 2.3%; 8
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Human adult heart
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                                         07-FEB-2001
                                                                         AAH11011 standard;
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ry Match 2.3%; Score
Local Similarity 50.3%; Pred.
                              (HELI-) HELIX RES INST
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(LABA/) LABAT I.
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er DNA marker #18996.
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Score 33.8; DB 5;
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No. 1.1e+02;
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                                                                                                             Human gene fra
JP10057062-A.
03-MAR-1998.
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18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence WO200255712-A2. 18-JUL-2002.
                                                                                                                                                                                      AAC38557 standard; DN
Arabidopsis thaliana
EP1033405-A2.
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                                                                                                                                                                                                                          Pseudomonas aeruginosa polynucleotide US6551795-B1.
22-APR-2003.
(GENO-) GENOME THERAPEUTICS CORP.
31Y MAICH 2.3%; Score 33.
11 Local Similarity 46.4%; Pred. No.
                                                       AAH03867 standard; cDNA; 765
Human cDNA clone (5'-primer)
                                                                                                                                           AAV15437 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ65930 standard; DNA;
Arabidopsis thaliana po
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                                     EP1074617-A2.
07-FEB-2001.
                                                                                                                                                                                                                                                                                    ABD17092 standard;
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                           (HELI-) HELIX RES INST.
                                                                                  (RIKA ) RIKAGAKU KENKYUSHO.
2.3%;
CY Match
Local Similarity 50.3%;
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HAAS W D.
GARCIA C A.
KRICKER M.
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LEDFORD B L.
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tag (EST)
                                                                                                                                  DNA; 753
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                                                                                                                                                                                                  DNA; 716 BP.
na DNA fragment
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Pred.
          Score 33.8; DB 4;
Pred. No. 1.4e+02;
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o. 1.3e+02;
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.3e+02;
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.4e+02;
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Arabidopsis thaliana DNA fragment SEQ ID NO:
EP1033405-A2.
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Plant transcription factor polynucleotide #811.
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HEARD J E.
RIECHMANN J L.
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RIECHMANN J L.
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILIGRIM M L.
DUBELL A N.
PINEDA O.
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MATHEW A V.

LEDFORD B L.

WOESSNER J P.
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GARCIA C A.
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No. 1.4e+02;
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.4e+02;
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RESULT 1487
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RESULT 1483
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RESULT 1482
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Gene #37 for inhibitory RNA
WO2003068961-A2.
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(RATC/)
(KUMI/)
(SHER/)
                                                                                                                                                  Human steroid-induced US6673549-B1.
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WO2003000898-A1.
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SARP 1 DNA.
WO200290992-A2.
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AAV60339 standard; cDNA; 1120 BP.
cDNA sequence of fibroblast growth factor-2 (FGF-2).
                                                                                                                                                                      ADL12563 standard; cDNA; 1004 BP.
Human steroid-induced C3A liver c
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                                                                                                                                                                                                                                                                                                                                           ADA69490 standard; DNA; 1002
Rice gene, SEQ ID 2813.
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ry Match 2.3%;
t Local Similarity 49.2%;
                                                                                                          (INCY-)
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h 2.3%; Score
Similarity 53.4%; Pred.
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RATCLIFFE O
KUMIMOTO R.
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h 2.3%; Score
Similarity 48.2%; Pred.
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Pred.
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Pred.
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                                                                NO 33
                                                                                                                                                                                                                                    33.8;
No. 1.
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No. 1.
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No. 1.
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No. 1.
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No. 1.
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1.4e+02;
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                                                                DB 12;
.6e+02;
                                                                                                                                                                                                                                    DB 8;
.6e+02;
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.5e+02;
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.5e+02;
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.4e+02;
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.5e+02;
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LEL-) CIBLEX CORP.

Lery Match

Best Local Similarity 5

RESULT 1490

ID AAA53563 standar

DE Human fibror

PN US608377

PD 04-7
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Best Local Similarity
RESULT 1496
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Best Local Similarity
RESULT 1498
ID ADA70200 standard;
DE Rice gene, SEQ ID 3
                                                                                                                                                                   Best Local Similarity
RESULT 1497
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Best Local Similarity
RESULT 1495
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Best Local Similarity
RESULT 1494
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Best I
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                                                                                                                                                                                                 Query Match
                                                           Query Match
                                                                                                                                                                                                                                                                                                          AAHI3860 standard; cDNA; 1809 BP.
Human cDNA sequence SEQ ID NO:10847.
EP1074617-A2.
07-PEB-2001.
(HELI ) HELIX RES INST.
Query Match
2.3%; Score 33.
Best Local Similarity 52.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS17400 standard; cDNA; 1120 BP. Full length cDNA for human fibroblast US6306613-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human fibroblast growth factor 2 cDNA. US6083706-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 1569 BP.
DNA encoding human alanine aminotransferase
WO200255712-A2.
18-JUI--7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-2004.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

23*; Score 33.8;

MARCH

2.3*; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP28745 standard; DNA; 1344 BP. Human secreted protein encoding WC2004035732-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP28744 standard; DNA; 1227 BP. Human secreted protein encoding sequence SEQ ID W02004035732-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA53563 standard; cDNA; 1120 BP.
                                                                                                                     ADR25867 standard; DNA; 1809 BP.
Breast cancer prognosis marker #1728.
WO2004065545-A2.
                                                                                                                                                                                                                              ADD18814 standard; DNA; 1809 BP.
Human disease related protein DNA sequence SeqID246.
WO2003018621-A2.
06-MAR-2003.
ADA70200 standard; DNA; 1980 BP.
Rice gene, SEQ ID 3523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIBL-) CIBLEX CORP.
                                             (ROSE-) ROSETTA INPHARMATICS LLC.
(NECA-) NETHERLANDS CANCER INST.
CAST SCOTT
TY MATCH 23%; SCOTT
Local Similarity 52.5%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LB-JUL-2002.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIVE-) FIVE PRIME THERAPEUTICS INC.

Ty Match 2.3%; Score 33.8;

Local Similarity 50.3%; Pred. No. 1.
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h 2.3%; Score 33.
Similarity 52.5%; Pred. No.
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Pred. No. 1.7e+02;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                            Score 33.8; DB 4;
Pred. No. 2.1e+02;
                                                Score 33.8; DB 13;
Pred. No. 2.1e+02;
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No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8; DB
No. 2e+02;
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.7e+02;
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.8e+02;
                                                                                                                                                                                         DB 10;
.1e+02;
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                                                                Length 1809;
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Query Match
Best Local Similarity
RESULT 1500
                                                                                                                                                                      Best Local Similarity RESULT 1499
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Best Local Similarity
                                                                                                                                                            WO2003000898-A1.
03-JAN-2003.
(SYGN) SYNGENTA PARTICIPATIONS AG.
(SYGN) SYNGENTA PARTICIPATIONS AG.
2.3%; Score 33.8;
Match 11arity 54.4%; Pred. No. 2.
                                   Gene sequence #SEQ ID 2646.
EP1258494-A1.
20-NOV-2000
                                                                                                                                    Rice gene conferring disease WO2003000906-A2.
                                                                                                                             03-JAN-2003
                                                                                                                                                         ADA48189 standard; DNA; 1980
                                                                                         (SYGN ) SYNGENTA PARTICIPATIONS

RY Match

Local Similarity 54.4%; Pre
             Match
                      CELLZOME AG.
 2.3%;
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resistance
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  33.8;
No. 2.
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No. 2.
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   DB 10;
.2e+02;
                                                                                            DB 9;
.2e+02;
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             Length 2000;
                                                                                                          1980;
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Run

BD099987 Novel

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Result
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Maximum |
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Perfect score:
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2: gb htg
3: gb in:
4: gb on
5: gb ov
6: gb ov
7: gb g
10: gb
11: q
13: '
14:
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(without alignments)
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Gapop 10.0 , Gapext 1.0
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AX135358
AX135358
AX35909
AX057789
BC009826
CQ85129
AX057789
BC009826
AX43091912
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AX454624 Sequence
AX491102 Sequence
AX697127 Sequence
AX697127 Sequence
AY359067 Homo sapi
BD159667 Primer fo
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AX882345

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AR337049

AK057789

BC009826

CQ851292

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Local Similarity
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      /organism="Homo sapiens"
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Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2 (lark, H.F., Gurney, A.I., Abaya, E., Baker, K., Baldwin, D., Brush, J. Chark, H.F., Gurney, A.I., Abaya, E., Currell, B., Deuel, B., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Chen, J., Chow, B., Chui, C., Crowley, C., Gu, Q., Hass, P.E., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Schoenfeld, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Goddard, A., Wood, W.I. and Godowski, P. Goddard, A., Wood, W.I. and Godowski, P. The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Protein Being the secreted and Transmembrane Prote
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                                                                                                                                                                                                                                                                A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 317); Catarrhini; Hominidae; Homo.
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishli, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primar for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 14510 09-UUL-2002;
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JUNICHI YAWAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAWATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
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28-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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 GGCAGGGAGCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCATCCTT
                                TCAGAAAGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCAGGC
                                                   CACTCTGAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTCCTTGG
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Primer for synthesizing full-length cDNA and use thereof.
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Homo sapiens (human)
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846

Query Match 98.5%; Score 1462.4; DB 6; Length 3375; Best Local Similarity 99.9%; Pred. No. 0; Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Dy 7 ACACGCAGGTAGCCGGAGCCCGGACCAGGCCCTGTGCCTCCTCCTCGTCGCGGG 66 1	Oy 67 TCCGCGAAGCCTGGAGCCGGGGAGCCCCGCGCTCGCCATGTCGGGGGGGCTCAGCAAC 126	Oy 127 AGGTTCCAAGGAGAAAGGCGTTCCACTCCAAAGCCCGCAGGAGAGGTGGCC 186	Qy 187 GAGATCAACGGGAGTTTCTGTGTCAACGAAGTACATGAAGAACCTTCCAGAA 246 DD 181 GAGATCAACCGGGAGCTTCTGTGTGACCAGAAGTACAGTGATGAAGAACCTTCCAGAA 240	QY 247 AAGCTCACAGCCTTCAAAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATT 306 DD 241 AAGCTCCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGACAATGAAGAGTT 300	Oy 307 GACCTGAIGTCTTTAAAGAGATGAIGAAAGCTTGGTGTCCCCAAGACCTGGAG 366	Oy 367 ATGAAGAAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCCAGAC 426	QY 427 TITGIGAACAIGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATTTGAA 486 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 487 GGABABAGCCBACGAGCAGCCCAAGCCAGTTGGCCCCCTCCAGAGAGACATTGCT 546	Qy 547 agccngcccrcaaaccccgccrcaaccrcccaaccrccccaraccrcccc 606 Db 541 agccrgcccrcaaaaccrccccaaacccrcccaacccccccc	Oy 607 ATCTTGCTGCCTTCTTGACACACTGTGATCTCTCTCTCTC	Oy 667 GGGTTTGTTTGTTCATCATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGG 726	Qy 727 CTCTGGGTCGGGGAATCCTGAGCCTTGGGTCCCCTCCTTCTTCTTCTTCCTCCTCCCCG 786	Qy 787 CTCCCTGTGCAGAGGCTGATATCAAACCAAAACTAGAGGGGGGGG	Oy 847 GAGGCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCCATCCTTTCAGAA 906	Oy 907 AGTCTCCAAGCTCAAGGTCACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCT 966 1	967 GAGAAGACCTTGGAGTAGGGCAGAGGCTGCAGGGCCTCTTCGGGTTTCCTTGGACAGTG 	1027 CCATGGTTCCAGTGCTCTGGTGTCACCCAGGACACACCCCCCTCGGGGGCCCCGGTGCCCCA
Qy 907 AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGACGAGGACCCCAGGCCACTCT 966	Qy 967 GAGAAGACCTTGGACGAGCAAGGCTGCAGGGCTCTTTCGGGTTTCCTTGGACAGTG 1026 Db 961 GAGAAGACCTTGGAGTAGGGACAGAGCTGCAGGCCTCTTTCGGGTTTCCTTGGACAGTG 1020	Qy 1027 CCATGGTTCCAGTGTCACCCAGGACACACACTCGGGGCCCCGCTGCCCCA 1086 Db 1021 CCATGGTTCCAGTGCTCTGGTGTCACCCCAGGACACACCACTCGGGGCCCCGCTGCCCCA 1080	Qy 1087 GCTGATCCCCACTCATTCCACACCTCTTCTCATCAGTGATGATGATGAGGAAGGA	Qy 1147 AGGAGCTTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTC 1206 Db 1141 AGGAGCTTGGCATTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTC 1200	Oy 1207 TCTGGCCACACCTGTGCAGGCAGCTGAGGCAGCGTGCAGCCCTACTGTCCCTTACTGG 1266	Qy 1267 GGCAGCAGAAGGCTGGAAGCCAGAAGTGAGGCCTGGGGTTTTGGGGGGAAAGGTCAGCTC 1326 Db 1261 GGCAGCAGAGGGCTTCGGAAGCAGAAGTGAGGCCTGGGGTTTTGGGGGGGAAAGGTCAGCTC 1320	Qy 1327 AGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGACCAGGATGGAGAATTAGGGAGTA 1386 Db 1321 AGTGCTGTTCCACCTTTTAGGGAGATACTGAGGGACCAGGATGGGAGAATGAGGAGTA 1380	Qy 1387 ABATGCTCACGCAAAGTCAGCAGCACACACACACACACACAC	Oy 1447 IGTCTGACCCCAATCTGCTTGAAA 1470 	T 8 339	LOCUS AX882339 3375 bp DNA linear PAT 17-DEC-2003 ACEESSION AX882339 GI:40037187 VERSION AX882339.1 GI:40037187	KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; CE 1 Secont., Isogai,T., Nishikawa,T RS Cta,T., Sugiyama,T., Wakamat	TITLE Primers for synthesising full-length clwa and their use JOURNAL Patent: BP 1074617-A 17244 07-FEB-2001; Research Association for Biotechnology (JP) FEATURES Location/Qualifiers	urce	CDS 100552 /note="unnamed protein product" /codon start=1 /www.tofan.ion.org.id=	/db_xref="G1:40037188" /translation="MSGELSNRFQGGKAFGLLKARQERRLAEINRELLCDQKYSDEEN LPEKLTAPPKEKKNREPDLNNEGEIDMSLKRAMBKLGVPKTHLEMKKMISEVTGGVSDT 1SYRDFVNMMIGKRSAVI,KIVMMFCKARNSSPKPVGDPPERDIASIL	ORIGIN

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Isogal, T. and Otsuki, T.

Direct Submission

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
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(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 GACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCCAAGACCCACCTGGAG 366
                                                                                                                                                                                               Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishiji, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.
      Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuronal
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precursor cells after 2-weeks retinoic acid (RA)
induction."
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0; Mismatches
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                                                                                                      Genet. 36 (1), 40-45 (2004)
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Matches 1463, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                       human cDNAs
                                                                                                         Nat. Gene
14702039
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                                     AGGAGCTTGGCATTGGGAGCCCTTCAAGAAGTACCAGAAGGAACCCTCCAGTCCTGCTC 1206
                                                                                                                                                                                                                                                                                                                                                                                                        TCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAGCGTGCAGCCCTACTGCCTTACTGG 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKO22845 3375 bp mRNA linear PRI 30-JAN-2004 Homo sapiens cDNA FLJ12783 fis, clone NT2RP2001876, moderately similar to ALLOGRAFT INFLAMMATORY FACTOR-1.
                                                                                                                                                                                                                                                                                                     1141 AGGAGCTTGGCATTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTC 1200
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAGCAGAGGCTTCGGAGGCCAGAAGTGAGGCCTGGGGTTTGGGGGGAAAGGTCAGCTC
                                                                                                                                                                                                                                                                                                                                                                   TCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAGCGTGCAGCCCTACTGTCCCTTACTGG
AK022845.1 GI:10434474
oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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KEYWORDS
SOURCE
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| Hillman, J.L., Lal, P., Tang, Y.Tom., Yue, H., Au-
| Corley, N.C., Guegler, K.J. and Baughn, M.R.
| Human immune system associated molecules
| Patent: US 6135941-A 16 24-OCT-2000;
| Location/Qualifiers
| Location/Qualifiers
| J. 3449 |
| /organism="unknown" | /mol_type="unassigned DNA"
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TITLE Compositions and methods relating to breast specific genes and protests (WO 0240672-A 29 23-MAY-2002; FEATURES Location/Qualifiers 1. 3470 / Organism="Homo sapiens" / Mmol_type="unassigned DNA" / Mb_xref="taxon:9606"	Query Match Best Local Similarity 99.7%; Pred. No. 0; Matches 1436; Conservative 0; Mismatches 3; Indels 1; Gaps 1;	Qy 3.2 CAGGGGCTGTGCTCCTCGTCCTCGCCGCGTCCGCGGGAGGCTGGAGCCGGGGGA 91	Oy 92 GCCCGGGGTCGCCATGTCGGGCGAGCTCAGCAACAGGTTCCAAGGAGGGAAGGCGTTCG 151	Oy 152 GCTTGCTCAAAGCCCGGCAGGAGGCTGGCCGAGATCAACCGGGAGTTTCTGTGTG 211	QY 212 ACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAGGTCACAGCCTTCAAAGAGAAGT 271 DD 182 ACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAAGCTCACAGACCTTCAAAGAGAAAGT 241	Oy 272 ACHIGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCTTTAAAGAGGATGA 331 Db 242 ACHIGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCTTTAAAGAGGATGA 301	OY 332 TGGAGAAGCTTGGTGTCCCCAAGACCTGGAGATGAAGAAGATGATCTCAGAGGTGA 391 ;	QY 392 CAGGAGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAACATGATGCTGGGGAAAC 451 Db 362 CAGGAGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAACATGATGCTGGGGAAAC 421	Oy 452 GGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCAACGAGAGCCCC 511	QY 512 AGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGAGGACCCCGCCTGG 571 bb 482 AGCCAGTTGGCCCCCCCCCCCCCCCCCGGAGAGACATTGCTAGCCTGCCCTGAGGACCCTGGG 541	Oy 572 ACTCCCCAGCCTTCCCCCATACCTCCCCCATCTTGCTGCCCTTCTTGACACACT 631	Oy 632 GIGATCICCICTCTCTCATTIGHTIGGCATTGAGGGTITGTTTGTTTTCATCATG 691 Db 602 GIGATCICTCTCTCTCTCTTTGTTTGGTCATTGAGGGTITGTTTGTTTTCATCAAIG 661		Qy 812 AAACCAAAAACTAGAGGGCAGGGCCAGGGCAGGCATCCAGCCTGTGTTCCCCTC 871 Db 782 AAACCAAAAACTAGAGGGGCAGGGCCAGGGCAGGGCTTCCAGCCTGTGTTCCCCTC 841 Qy 872 ACTTGGAGGAACCAGGCTCCCATCCTTTCAGAAAGTCTCCAAGCTCA 931 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
	OY 787 CTCCCTGTGCAGAAGGGCTGATATCAAACCTAGAGGGGGGGG	Qy 847 GAGGCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAA 906	OY 907 AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGAGGAGGACCCCAGGCCACTCT 966	OY 967 GAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTG 1026	Qy 1027 CCATGGTTCCAGTGTCACCCAGGACACAGGCCACTCGGGGCCCCGCTGCCCCA 1086 bb 1020 CCATGGTTCCAGTGTCACCCAGGACACAGGCCACTCGGGGCCCCGCTGCCCCA 1079	Oy 1087 GCTGATCCCCACTCATTCCACACCTCTTCTCACTCAGGATGAGGTGGGGAAGGA 1146 Db 1080 GCTGATCCCCACTCATTCCACACCTCTTCTCAGTGATGTGAAGTGGGAAGGAA	Qy 1147 AGGAGCTTGGCATTGGGAGCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTC 1206 Db 1140 AGGAGCTTGGCATTGGGAGCCTTCAAGAAGGTACCAGAAGGAACCTCCAGTCCTGCTC 1199	QY 1207 TCTGGCCACACCTGTGCAGGCAGGCAGAGCAGCGTGCAGCCCTACTGTCCCTTACTGG 1266 Db 1200 TCTGGCCACACCTGTGCAGCAGCTGAGAGCGAGCGTGCAGCCCTACTGTCCCTTACTGG 1259	Qy 1267 GGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTGGGGTTTGGGGGGAAAGGTCAGCTC 1326 Db 1260 GGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTGGGGTTTGGGGGGAAAGGTCAGCTC 1319	Qy 1327 AGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGACCAGGATGGGAGAATGAGGAGTA 1386 Db 1320 AGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGACCAGGATGGGAGAATGAGGAGTA 1379	OY 1387 AAATGCTCACGGCAAAGTCAGCACACTGGTAAGCCAAGACTGAGAAATACAAGGTTGCT 1446 Db 1380 AAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGACTGAGAATACAAGGTTGCT 1439	Oy 1447 TGTCTGACCCCAATCTGCTTGAAA 1470 Db 1440 TGTCTGACCCCAATCTGCTTGAAA 1463	RESULT 11 AX430949 AX430949 BECUGUS DEFINITION Sequence 29 from Patent W00240672. ACCESSION AX430949 VERSION AX430949 KRYWORDS	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Recipon, H., Liu, C., Salceda, S., Sun, Y. and Cafferkey, R.

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13899240.
Location/Qualifiers
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  Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadar@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14714398.
Contact: MGC help desk
Email: cgapbs-readil.nih.gov
Tissue Procurement: ATCC
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llarity 99.6%; Pred. No. 0;
Conservative 0; Mismatches
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Direct Submission
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1. (bases 1 to 1446)

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, F., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Bouffard, G.G., Blakesley, R.W., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Young, A.C., Shevchenko, Y.,
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HOWO Sapiens chromosome 9 open reading frame 58, mRNA (cDNA clone IMAGE:3842109), partial cds.
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841 AGAGGGGCAGGCCAGGGCAGGCATCCCAGCCTGTGTTCCCCCTCACTTGGAGGAAC 900
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KEYWORDS
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Db 1261 GGTAGAAGTGAGGCTTGGGGGAAAGGTCACTCTGTGTGTTCCACCTTTT 1320 Oy 1345 AGGGAAGGTACTGAGGGGTTTTGGGGGGAAAGGTCAGTCTCCACCTTTT 1320 Db 1321 AGGGAAGGTTACTGAGGGGACCAGGATGAGAGAAATGGTCACGGCAAAGT 1404 1321 AGGGAGGTTACTGAGGGGACCAGGATGAGGAGTAAAATGCTCACGGCAAAGT 1380 Oy : 1405 CAGCAGCATACTGAGGGGACCAGGAATACAAGGTTAGTTGTCTGA 1453 Db 1381 CAGCAGCATGGTAAGCCAAGACTGAGAATACAAGGTTAGTTGTCTGA 1429 RESULT 14 CQ881292 CQ88	Patent: EP 1447413-A 1761 18-AUG-2004; Research Association for Biotechnology (JP) Location/Qualifiers 13451 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 22.6%; Score 1374.4; DB 6; Length 3	Best Local S Matches 1463 7 1	CCGCGAAAGCTGGGGCGGGGGGGGGGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCAAC	Db 181 dadatchacceracereagaagaagacceraceragargartrcafetrccag 240 Qy 198	Oy 289 AACAATGAAGGGAGATTGACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTC 348
206 TGTGTGACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAGGTCACAGGCTTCAAAG 265 181 TGTGTGACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAAGGTCACAGCCTTCAAAG 240 266 AGAAGTACATGGAGTTTGACCTGAACAATGAAGAATGACCTGATGCTTTTAAAGA 325 241 AGAAGTACATGGAGTTTGACCTGAACAATGAAGGAATTGACCTGATGTCTTTAAAGA 325 326 GGATGATGGAGTTTGACCTGAACAATGAAGGAGATTGACCTGATGTCTTTAAAGA 300 326 GGATGATGGAGGTTTGACCTGAACAATGAAGGATTGACCTGATGTCTTTAAAGA 300 327 GGAAGTACATGGAGTTTGACCTGAACAATGAAGAATGACCTGATGTTTTAAAGA 300 328 AGGTGACAGAGAGATTGGTGCCCCAAGACCCACTGGAGATGAAGAATGATCTCAG 360 381 AGGTGACAGGAGAGACTTGGTGACTATTGCTACCGAGATGAAGATGATGTCTCAG 360 382 AGGTGACAGGAGAGACACTATATCCTACCGAGACTTTGTGAACATGATGCTGG 420 446 GGAAACGGTCGGCTCACAGTTAATCCTACCGAGACTTTGTGAACATGATGCTGG 420 446 GGAAACGGTCGGCTCCTCAAGTTAATCCTACCGAGACTTTGTGAACATGATGCTGGGAGAGA 480 481 GGCACCAAGCCTCCTCCAAGTTAATCCTACATTGAAGAAAAACCCAAGAGAGA 480 566 GCCCCAAGCCGTTGGCCCCTCCAGAGAGAATTGATGCTGCCCTGAGGAGCCC 565 [TTTCA TTTCA TTTCA ATCCT ATCCT	GAGCCTTGGGTCCCCTCCTCTTCTTCCTCCTCCTTCCCGCTCCTGTGCAAAGGGCT GATATCAAACCAAAAACTAGGGGGGGGGG	866 CCCCTCACTTGGAGGAACCACCACTCTCCATCCTTTGGAAAGTCTCCAAGCCAAGTTCA 925 1	961 GACAAGGCTGCAGGGCCTTTCGGGTTTCCTTGGACAGTGCCATGGTCTCTG 1020 1046 GTGTCACCCAGGACACACACTCGGGGCCCCGGTGCCCAGTGGTCTCTTCC 1105 1051 GTGTCACCCAGGACACACACACACACACACACACACACAC	

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Db 1261 AV Qy 1249 CC Db 1321 CC Qy 1309 GC	Qy 1369 A;	Search completed			
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